

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Inc.  
October 24, 2004, 14:02:27 ; Search time 51.308 Seconds  
(without alignments)  
699,375 Million cell updates/sec  
in search, using sw model

Title:	US-10-661-784-3
Prefect Score:	687
Sequence:	1 GSGIDPVQDPPTKICVGCPRD.....VPWEEKKIYPTVTVNKHCEP 127
Scoring table:	BLOSUM62
Gappen:	Gapop 10.0 , Gapext 0.5
Searched:	1586107 BQS, 282547505 residues
Total number of hits satisfying chosen parameters:	
	1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0.  
Maximum Match 1.0<sup>t</sup>  
Listing first 45 summaries

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A_GenSeq_29Jan04:*
 1: GenSeqCP1900s:*
 2: GenSeqCP1900s:*
 3: GenSeqCP2000s:*
 4: GenSeqCP2001s:*
 5: GenSeqCP2001s:*
 6: GenSeqCP2003ab:*
 7: GenSeqCP2003bb:*
 8: GenSeqCP2004s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
					Start	End
1	618	90.0	123	3	AAY95426	Human big
2	618	90.0	304	6	ABP70801	Human ext
3	618	90.0	322	6	ABP70799	Human pro
4	618	90.0	323	6	ABP92044	Human pro
5	618	90.0	358	6	ABP70800	Human ext
6	618	90.0	390	6	ABP99149	Novel hum
7	618	90.0	398	6	ABP99143	Novel hum
8	618	90.0	427	8	ADD76884	Human pro
9	618	90.0	615	6	ABP99144	Novel hum
10	618	90.0	626	5	ABP78707	Human big
11	618	90.0	644	4	ABG21101	Novel hum
12	618	90.0	644	5	ABP78710	Human big
13	618	90.0	644	6	ABP99150	Novel hum
14	618	90.0	644	6	ABP99145	Novel hum
15	585	82.3	122	3	ABP7447	Human kin
16	585	82.3	435	4	ABG11105	Novel hum
17	556.5	81.0	117	2	ABR33350	Domains 3
18	440	64.0	436	1	ABP0257	Bradykinin
19	413	60.1	434	1	ABP10633	Bradykinin
20	411	59.8	357	6	ABR1202	Human DIT
21	388	56.5	235	5	ABG0077	Ruman DIT
22	320.5	46.7	248	4	ABG21102	Novel hum
23	316	46.0	369	4	ABP21099	Novel hum
24	316	46.0	369	4	ABG21100	Novel hum
						redundant

September 24, 2004, 14:02:27 ; Search time 51.308 Seconds  
[without alignment] ;  
for 175 million cell updates/sec

US-10-661-784-3  
687  
Title: perfect score!  
perfect score!

Scoring table: BL2USUM62 Gapcp 10.0 , Gapext 0.5

1586107 searched; 1586107 hits satisfying chosen parameters;  
28347505 residues; 1586107 BCGs.

minimum DB sec length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_29Jan04;\*  
1\_genescqp1980s;\*  
2\_

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3: genesetP20006;*
4: genesetP20016;*
5: genesetP20026;*
6: genesetP20036;*
7: genesetP2003b6;*
8: genesetP20046;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALL CATEGORIES

**RESULT 1**  
AAV95426  
ID AAV95426 standard; Peptide; 123 AA.

AAV95426;  
25-SEP-2000 (First entry)  
Human high mol.wt. kininogen domain 3.  
Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;  
endothelial cell proliferation; apoptosis; cancer; ocular disorder;  
rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy;  
human; D3 peptide.

OS Homo sapiens.  
 XX WO200035407-A2.  
 PN 22-JUN-2000.  
 PD XX  
 XX 05-DEC-1999; 9990-US028465.  
 PR XX 16-DEC-1998; 98US-0112427P.  
 XX (ITEM ) UNIV TEMPLE.  
 PA (NCCR/) MCCRAE R K.  
 PA XX  
 PI McCrae RK;  
 XX DR WPI: 2000-442247/38.  
 XX PT Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, pain, arthritis, and ocular disorders comprising a kininogen domain 3 analog.  
 PT XX  
 PT XX  
 PT XX  
 PT XX  
 PS Disclosure; Page 4; 44pp; English.  
 PS XX  
 CC The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see A9y95405-24) that are  
 CC analogues of certain sites in the HK domain 3, specifically Asn75-Tyr76, Cys249-Lys318 and Tyr399-Ser314. The peptides, in  
 CC which native Cys residues may be replaced by Ala residues, inhibit  
 CC endothelial cell proliferation and may also induce endothelial cell  
 CC apoptosis. Compositions including the peptides are used in claimed  
 CC methods for inhibiting angiogenesis, inhibiting endothelial cell  
 CC proliferation, inducing apoptosis in endothelial cell, and treating  
 CC cancer, pain, arthritis, and ocular disorders comprising a kininogen domain 3  
 CC analog.

CC rheumatoid arthritis, and ocular disorders characterized by undesired  
 CC vascularization of the retina are treated  
 XX Sequence 123 AA;  
 SQ Query Match Score 618; DB 3; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 5; se-63;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GKDYQPPRKICGCPDIPNSPHEARELTHTKINAENNATYFKIDDNVKARYQVY 62  
 Db 1 GKDYQPPRKICGCPDIPNSPHEARELTHTKINAENNATYFKIDDNVKARYQVY 60  
 Qy 63 AGKRYFIDFVARETTCSESNEELTESCTKLQGSLDCNAEVYVPMWKIYPTV 118  
 Db 61 AGKRYFIDFVARETTCSESNEELTESCTKLQGSLDCNAEVYVPMWKIYPTV 116  
 Qy 64 AGKRYFIDFVARETTCSESNEELTESCTKLQGSLDCNAEVYVPMWKIYPTV 245

RESULT 2  
 ABP70801 ID ABP70801 standard; protein, 304 AA.  
 XX AC ABP70801;  
 XX DT 26-AUG-2003 (first entry)  
 DB Human extracellular messenger, EXMES-26.  
 KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;  
 KW endocrine disorder; cancer.  
 OS Homo sapiens.  
 XX PN WO2003018612-A2.  
 PD 06-MAR-2003.  
 XX PP 22-AUG-2003.  
 XX PR 24-AUG-2001; 2001US-0314611P.  
 PR 14-DEC-2001; 2001US-0314584P.  
 PR 18-JAN-2002; 2002US-03150595P.  
 PR 11-MAR-2002; 2002US-0316332P.  
 PR 15-MAR-2002; 2002US-0316407P.  
 PR 05-APR-2002; 2002US-0370761P.  
 PR 24-JUN-2002; 2002US-0391378P.  
 PA (INCYT- INCYTE GENOMICS INC.  
 XX DR WPI; 2003-278643/27.  
 DR N-PSDB; ACC42386.  
 XX PS Claim 1, Page 207, 224pp, English.  
 XX PT New human extracellular messenger (EXMES) polypeptide, useful for  
 PT preparing a composition for treating a disease associated with decreased  
 PT expression or overexpression of functional EXMES e.g. autoimmune  
 PT disorders or cancer.  
 XX PT The present invention relates to novel human extracellular messenger  
 CC proteins (EXMES-1 to-28, ABP7074-ABP70801) and their coding sequences  
 CC (ACC42361-ACC43188). The proteins are useful for preparing a composition  
 CC for diagnosing or treating a disease or condition associated with  
 CC decreased expression or overexpression of functional EXMES e.g.  
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or  
 CC cancer  
 XX SQ Sequence 304 AA;

XX Query Match Score 618; DB 6; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GKDYQPPRKICGCPDIPNSPHEARELTHTKINAENNATYFKIDDNVKARYQVY 62  
 Db 130 GKDYQPPRKICGCPDIPNSPHEARELTHTKINAENNATYFKIDDNVKARYQVY 189  
 Qy 63 AGKRYFIDFVARETTCSESNEELTESCTKLQGSLDCNAEVYVPMWKIYPTV 118  
 Db 190 AGKRYFIDFVARETTCSESNEELTESCTKLQGSLDCNAEVYVPMWKIYPTV 245

RESULT 3  
 ABP70799 ID ABP70799 standard; protein, 322 AA.  
 XX AC ABP70799;  
 XX DT 26-AUG-2003 (first entry)  
 XX DE Human extracellular messenger, EXMES-26.  
 KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;  
 KW endocrine disorder; cancer.  
 OS Homo sapiens.  
 XX PN WO2003018612-A2.  
 PD 06-MAR-2003.  
 XX PP 22-AUG-2002; 2002WO-US0307213.  
 XX PR 24-AUG-2001; 2001US-0314811P.  
 PR 14-DEC-2001; 2001US-034584P.  
 PR 18-JAN-2002; 2002US-035595P.  
 PR 15-MAR-2002; 2002US-036432P.  
 PR 05-APR-2002; 2002US-0364607P.  
 PR 24-JUN-2002; 2002US-0391378P.  
 PA (INCYT- INCYTE GENOMICS INC.  
 XX DR Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS;  
 PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;  
 PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebradjian Y;  
 PI Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;  
 PI Ramkumar J;  
 XX DR WPI; 2003-278643/27.  
 DR N-PSDB; ACC42386.  
 XX PS Claim 1, Page 207, 224pp, English.  
 XX PT The present invention relates to novel human extracellular messenger  
 CC proteins (EXMES-1 to-28, ABP7074-ABP70801) and their coding sequences  
 CC (ACC42361-ACC43188). The proteins are useful for preparing a composition  
 CC for diagnosing or treating a disease or condition associated with  
 CC decreased expression or overexpression of functional EXMES e.g.  
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or  
 CC cancer  
 XX SQ Sequence 322 AA;

Query Match Score 618; DB 6; Length 322;  
 Best Local Similarity 90.0%; Pred. No. 2.1e-62;  
 Matches 0, Mismatches 0, Indels 0, Gaps 0;

Qy 3 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 62  
 Db 148 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 207  
 Qy 63 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 118  
 Db 208 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 263

RESULT 4  
 ABU92044 standard; protein; 329 AA.  
 ID ABU92044;  
 XX AC ABU92044;  
 DT 15-JUL-2001 (first entry)  
 DB Human protein modification and maintenance molecule-24 (PMM-24).  
 XX Human; protein modification and maintenance molecule-24 (PMM-24).  
 KW cell proliferation disorder; atherosclerosis; neurological disorder;  
 KW epilepsy; Huntington's disease; stroke; immune disorder; allergy;  
 KW inflammatory disorder; AIDS; developmental disorder; hypothyroidism;  
 KW Cushing's syndrome; Gastrointestinal disorder; epithelial disorder;  
 KW infection; cytosstatic; antiarteriosclerotic; anticonvulsant; nootropic;  
 KW neuroprotective; cerebroprotective; anti-HIV; antiallergic; pulmonary;  
 KW antiinflammatory; thyromimetic.  
 OS Homo sapiens.  
 XX WO2003031939-A2.  
 PN XX  
 PD 17-APR-2003.  
 XX PP 11-OCT-2002; 2002WO-US032850.  
 PR 12-OCT-2001; 2001US-0329689P.  
 PR 25-OCT-2001; 2001US-0335703P.  
 PR 09-NOV-2001; 2001US-0348887P.  
 PR 28-NOV-2001; 2001US-0334145P.  
 PR 06-DEC-2001; 2001US-03347451P.  
 PR 14-DEC-2001; 2001US-03340584P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX Rankumar J, Gorval AE, Baughn MR, Emerling BM, Yang J, Lee SY;  
 PI Tran UK, Becha SD, Dugan BM, Lee EA, Griffin JA, Li JX;  
 PI Spargue WW, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AB, Yue H;  
 PI Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;  
 PI Bhattacharji U, Burrell JD, Lee S, Blake JJ, Ho A, Zheng W;  
 DR WPI: 2003-410274/40.  
 DR N-PSDB; ACA2439.

CC polynucleotides. The diseases or conditions associated with decreased expression or overexpression of PMM are cell proliferation disorders (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders (e.g. allergies), developmental disorders (e.g. hypothyroidism, Cushing's syndrome), gastrointestinal or epithelial disorders, and infections. The PMM polypeptides and their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in CC specifically bind to, or modulate the activity of the polypeptide. CC ABU92044-ABU92060 represent the human PMM polypeptides of the invention.

Query Match Score 618; DB 6; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-62;  
 Matches 0, Mismatches 0, Indels 0, Gaps 0;

Qy 3 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 62  
 Db 155 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 214  
 Qy 63 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 118  
 Db 215 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 270

Sequence 329 AA;

Query Match Score 618; DB 6; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-62;  
 Matches 116, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Qy 3 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 62  
 Db 155 GKDYQPPTKIVCPDIPNSPELEBTUTTITLNAAENNATYPKIDVNYKRVQVV 214  
 Qy 63 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 118  
 Db 215 AGKKCFIDFVARETCSKESNEELTECETKGGSQLDNAEVTVPMEKKIYPTV 270

RESULT 5  
 ABP70800  
 ID ABP70800 standard; protein; 358 AA.  
 XX AC ABP70800;  
 XX DT 26-AUG-2003 (first entry)  
 XX DB Human extracellular messenger, EXMES-27.  
 XX KW Human; extracellular messenger; EXMES; cyrostatic; antidiabetic; diabetes;.  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; cancer.  
 KW endocrine disorder; cancer.  
 XX OS Homo sapiens.  
 XX DB Human extracellular messenger, EXMES-27.  
 XX PN WO2003018612-A2.  
 XX PD 06-MAR-2003.  
 XX PR 22-AUG-2002; 2003WO-US027213.  
 PR 24-AUG-2001; 2001US-0314811P.  
 PR 14-DEC-2001; 2001US-0314811P.  
 PR 18-JAN-2002; 2002US-0350535P.  
 PR 11-MAR-2002; 2002US-0363322P.  
 PR 06-DEC-2002; 2002US-0364070P.  
 PR 05-APR-2003; 2003US-0370561P.  
 PR 24-JUN-2002; 2002US-031378P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walia NK, Elliott VS, Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Trang IT, Burford N, Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardian Y, Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM; Ramkumar J;  
 XX WPI: 2003-278643/27.  
 DR DR N-PSDB; ACC4387.

CC New human extracellular messenger (EXMES) polypeptide, useful for PT preparing a composition for treating a disease associated with decreased PT expression or overexpression of functional EXMES e.g. autoimmune PT disorders or cancer.

CC The present invention relates to the isolation of human protein PT modification and maintenance molecules (PMM), and the Polynucleotide PT sequences encoding them. A total of 40 PMM polypeptides (designated PMM PT -1 to PMM-40) are disclosed. The sequences of the invention are useful PT for diagnosing a condition or disease associated with the expression of PMM in a subject, preparing a polyclonal or monoclonal antibody, and PT generating an expression profile of a sample containing the

PS Claim 1; Page 206; 220pp; English.

XX The present invention relates to novel human extracellular messenger

CC proteins (EXNBS-1 to -28; ABP70774-ABP70801) and their coding sequences

CC (ACC42361-ACC42398). The proteins are useful for preparing a composition

CC for diagnosing or treating a disease or condition associated with

CC decreased expression or overexpression of functional EXNBS e.g.

CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or

CC cancer

XX

QQ Sequence 358 AA;

Query Match 90.0%; Score 618; DB 6; Length 358;

Best Local Similarity 100.0%; Pred. No. 2.4e-62;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GKDQPPKIKVGCRDIPNSPBLTHTTTLKAAENATTYFKIDDNVKARVQVV 62

Db 184 GKDQPPKIKVGCRDIPNSPBLTHTTTLKAAENATTYFKIDDNVKARVQVV 243

Oy 63 AGKXYPIDFVARETCSKESNBELTECSTKLGSIDCNAEVTVWPWCKYPT 118

Db 244 AGKXYPIDFVARETCSKESNBELTECSTKLGSIDCNAEVTVWPWCKYPT 299

RESULT 6

ID ABU99149 standard; protein; 390 AA.

AC ABU99149;

XX DT 01-AUG-2003 (first entry)

DE Novel human GPCR related protein NOV129.

XX Human: G-protein coupled receptor related protein; GPCR related protein;

KW NOV; cytosolic; cardiac; antiatherosclerotic; antidiabetic;

KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;

KW antiparkinsonian; neuroprotective; nortropic; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;

KW diabetes; immune disorder; AIDS; obesity; asthma;

KW haemopoietic disorder; Parkinson's disease; Alzheimer's disease;

KW infection; multiple sclerosis; cancer-associated cachexia;

KW wasting disorder; chronic disease; neurogenesis; cell differentiation;

KW cell proliferation; haemopoiesis; wound healing; angiogenesis;

KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

OS W0200299116-A2.

PN 12-DEC-2002.

PP 04-JUN-2002; 2002WO-US017428.

XX

PR 04-JUN-2001; 2001US-025607P.

PR 04-JUN-2001; 2001US-025661P.

PR 06-JUN-2001; 2001US-026404P.

PR 14-JUN-2001; 2001US-02885P.

PR 15-JUL-2001; 2001US-028856P.

PR 21-JUN-2001; 2001US-029949P.

PR 26-JUN-2001; 2001US-0300881P.

PR 28-JUN-2001; 2001US-031550P.

PR 13-AUG-2001; 2001US-03197P.

PR 29-AUG-2001; 2001US-035071P.

PR 14-SEP-2001; 2001US-032229P.

PR 17-SEP-2001; 2001US-032705P.

PR 14-DEC-2001; 2001US-034118P.

PR 28-FEB-2002; 2002US-03118P.

PR 12-MAR-2002; 2002US-033367P.

PR 12-MAR-2002; 2002US-034367P.

PR 03-JUN-2002; 2002US-00363676.

XX (CURA+) CURAGEN CORP.

PA XX

PI Anderson DW, Baumgartner JC, Boldog PL, Casman SJ, Edinger SR, Gangolli EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Keruda R, Li L, Macdougall JR, Malynkar UM, Milliet I, Padigaru M, Patterson M, Pena CEA, Resarelli L, Shimkets RA, Stora DJ, Sptekal KA, Voss EZ, Zethusen BD;

XX

DR WPI; 2003-140627/13.

DR N-PSDB; ACD03653.

XX

FT New NOVX polypeptides and nucleic acids, useful for preventing or

FT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,

FT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

FT pharmacogenomics.

XX

PS Claim 1; Page 147; 332pp; English.

XX

CC The invention describes an isolated polypeptide (I) comprising any of 27

CC 118-961 residue amino acid sequences, given in the specification, a

CC mature form of them, a sequence having at least 95 % identical to them,

CC or a sequence having one or more conservative substitutions in them. The

CC polypeptide is useful in manufacturing a medicament for treating a

CC syndrome associated with a human disease selected from a pathology

CC associated with the polypeptide. The NOVX polypeptides, polynucleotides

CC and antibodies are useful in treating or preventing NOVX associated

CC disorders. e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune

CC disorders, AIDS, obesity, asthma, hemopoietic disorders, Parkinson's

CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-

CC associated cachexia, and other wasting disorders associated with chronic

CC diseases. The nucleic acids and polypeptides may also be used as targets

CC for the identification of small molecules that modulate or inhibit e.g.

CC neurogenesis, cell differentiation, cell proliferation, haemopoiesis,

CC wound healing and angiogenesis, in gene therapy, in generation of

CC antibodies that bind immunospecifically to NOVX substances for use in

CC therapeutic or diagnostic methods. The nucleic acids are further used as

CC hybridisation probes, in chromosome mapping, tissue typing, preventive

CC medicine, and pharmacogenomics. The polypeptides are also useful as

CC vaccines. This is the amino acid sequence of a novel human G-protein

CC coupled receptor related protein NOV

XX

SO Sequence 390 AA!

Query Match 90.0%; Score 618; DB 6; Length 390;

Best Local Similarity 100.0%; Pred. No. 2.7e-62;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GKDQPPKIKVGCRDIPNSPBLTHTTTLKAAENATTYFKIDDNVKARVQVV 62

Db 216 GKDQPPKIKVGCRDIPNSPBLTHTTTLKAAENATTYFKIDDNVKARVQVV 275

Oy 63 AGKXYPIDFARETCSKESNBELTSCEKLGOLDNAEVVPMEKYPTV 118

Db 276 AGKXYPIDFARETCSKESNBELTSCEKLGOLDNAEVVPMEKYPTV 331

RESULT 7

ID ABU99143

AC ABU99143 standard; protein; 398 AA.

XX

DB 01-AUG-2003 (first entry)

XX

DE Novel human GPCR related protein NOV129.

XX

KW Human; G-protein coupled receptor related protein; GPCR related protein;

KW NOV; cytosolic; cardiac; antiarteriosclerotic; antidiabetic;

KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;

KW antiparkinsonian; neuroprotective; nortropic; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;



CC liver disorder.  
 XX Sequence 427 AA;  
 50 Query Match 90.0%; Score 618; DB 8; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 3 1e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GDDFQPPPKICVGCPRDIPNTSPLLEETLTHITLNAENNATYFKIDNVKCKARYQVV 62  
 Db 253 GKDvQPPPKICVGCPRDIPNTSPLLEETLTHITLNAENNATYFKIDNVKCKARYQVV 312  
 Qy 63 AGKXPFIDPVAEETTCSKESEBLLTBSCETKQASLDCKNAEVYYVPWZKLIPTV 118  
 Db 313 AGKXPFIDPVAEETTCSKESEBLLTECSTKQASLDCKNAEVYYVPWZKLIPTV 368

RESULT 9  
 ABU99144  
 ID ABU99144 standard; protein; 615 AA.  
 AC ABU99144;  
 DT 01-AUG-2003 (first entry)  
 XX Novel human GPCR related protein NOV12B.  
 XX Human; G-protein coupled receptor related protein; GPCR related protein;  
 NOV; cytosolic; cardiac; antiatherosclerotic; antiidiabetic;  
 immunomodulator; anti-HIV; anorectic; antilasthmatic; haemostatic;  
 anti-parkinsonian; neuroprotective; nootropic; gene therapy; vaccine;  
 NOV-associated disorder; cardiomyopathy; atherosclerosis; cancer;  
 diabetes; immune disorder; AIDS; obesity; asthma;  
 hematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
 infection; multiple sclerosis; cancer-associated cachexia;  
 wasting disorder; chronic disease; neurogenesis; cell differentiation;  
 cell proliferation; haematozoies; wound healing; angiogenesis;  
 chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.  
 XX Homo sapiens.  
 OS WO200299116-A2.  
 XX PD 12-DEC-2002.  
 XX PP 04-JUN-2002; 2002WO-US017428.  
 PR 04-JUN-2001; 2001US-0295607P.  
 PR 04-JUN-2001; 2001US-0295610P.  
 PR 06-JUN-2001; 2001US-02956104P.  
 PR 06-JUN-2001; 2001US-02956118P.  
 PR 14-JUN-2001; 2001US-02956285P.  
 PR 15-JUN-2001; 2001US-0295656P.  
 PR 21-JUN-2001; 2001US-0295649P.  
 PR 26-JUN-2001; 2001US-0300838P.  
 PR 28-JUN-2001; 2001US-031550P.  
 PR 13-AUG-2001; 2001US-0311972P.  
 PR 27-AUG-2001; 2001US-0315701P.  
 PR 14-SEP-2001; 2001US-031560P.  
 PR 17-SEP-2001; 2001US-0322293P.  
 PR 14-DEC-2001; 2001US-034186P.  
 PR 28-FEB-2002; 2002US-0361189P.  
 PR 12-MAR-2002; 2002US-0361673P.  
 PR 03-JUN-2002; 2002US-0361676P.  
 PR 03-JUN-2002; 2002US-0361676.

PI Voss EZ; Zerhusen BD;  
 XX WPI; 2003-146627/13.  
 DR N-SPSB; ACD0648.  
 XX PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, tissue typing or  
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX Claim 1; Page 144; 332PP; English.  
 XX  
 CC The invention describes an isolated polypeptide (1) comprising any of 27  
 CC 118-961 residue amino acid sequences, given in the specification, a  
 CC mature form of them, a sequence that is at least 95 % identical to them,  
 CC or a sequence having one or more conservative substitutions in them. The  
 CC polypeptide is useful in manufacturing a medicament for treating a  
 CC syndrome associated with a human disease selected from a pathology  
 CC associated with the polypeptide. The NOVX polypeptides, polynucleotides  
 CC and antibodies are useful in treating or preventing NOVX-associated  
 CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
 CC disorders, AIDS, obesity, asthma, haematopoietic disorder, Parkinson's  
 CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
 CC associated cachexia, and other wasting disorders associated with chronic  
 CC diseases. The nucleic acids and polypeptides may also be used as targets  
 CC for the identification of small molecules that modulate or inhibit e.g.  
 CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
 CC antibodies that bind immunospecifically to NOVX substances for use in  
 CC therapeutic or diagnostic methods. The nucleic acids are further used as  
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
 CC medicine, and pharmacogenomics. The polypeptides are also useful as  
 CC vaccines. This is the amino acid sequence of a novel human G-protein  
 CC coupled receptor related protein NOV  
 XX SQ Sequence 615 AA/  
 Query Match 90.0%; Score 618; DB 6; Length 615;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 YY 3 GKDvQPPKICVGCPRDIPNTSPLLEETLTHITLNAENNATYFKIDNVKCKARYQVV 62  
 Db 224 GKDvQPPKICVGCPRDIPNTSPLLEETLTHITLNAENNATYFKIDNVKCKARYQVV 283  
 Qy 63 AGKXPFIDPARETCSKESNEELTBSCETKQASLDCKNAEVYYVPWZKLIPTV 118  
 YY 63 AGKXPFIDPARETCSKESNEELTBSCETKQASLDCKNAEVYYVPWZKLIPTV 118  
 Db 284 AGKXPFIDPARETCSKESNEELTBSCETKQASLDCKNAEVYYVPWZKLIPTV 339  
 RESULT 10  
 ABP78707  
 ID ABP78707 standard; protein; 626 AA.  
 XX AC ABP78707;  
 XX DT 18-JUL-2002 (first entry)  
 XX Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.  
 XX Human; kininogen; high molecular weight kininogen; HK; D5 domain;  
 KW D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;  
 KW antiatherosclerotic; vasotrophic; vulnerary; tranquilliser; thrombolytic;  
 KW ophthalmological; synacological; antiulcer; antidiabetic; antiarthritic;  
 KW antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.  
 XX OS Homo sapiens.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Anderson DW, Baumgartner JC, Boldog PL, Casman SJ, Edinger SR, Ganguli EP, Gerlach UJ, Gorman L, Guo X, Hjalt T, Kekuda R, Li L, Macdougall JR, Mayanjan TN, Millet I, Padigaru M, Paturajan M, Pena CEA, Rastelli L, Shimkets RA, Stone DJ, Spitek KA, Vernet CAM,  
 PI Key, FT Domain  
 PI Location/Qualifiers  
 PI 38.; '508 /label= D5\_domain  
 PN WO200214369-A2.

XX PD 21-PFB-2000.  
 XX PF 24-JUL-2001; 2001WO-US023185.  
 XX PR 24-JUL-2000; 2000US-0220194P.  
 XX PA (ATTB-) ATTENDON LLC.  
 XX PI Mazar AP, Juarez JC,  
 XX WPI; 2002-39361/42.  
 XX Novel human kininogen DS domain polypeptides useful for treating  
 PT conditions associated with endothelial cell migration, proliferation,  
 PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign  
 PT hyperplasia.  
 XX Disclosure: Page 13; 84pp; English.  
 CC The present invention describes an isolated polypeptide (I) that  
 CC corresponds to the DS domain of human kininogen, or biologically active  
 CC peptide fragment, homologue or functional derivative, and which: (a)  
 CC inhibits angiogenesis; (b) binds to the DS binding site on endothelial  
 CC cells (EC); (c) activates signalling pathways leading to the introduction  
 CC of apoptosis in EC; and/or (d) inhibits the signalling pathway required  
 CC for maintenance of EC viability. (I) has cyostatic, antitumour,  
 CC antiatherosclerotic, vasodilator, tranquiliser, thrombolytic,  
 CC ophthalmological, symptomatic, antiarthritic, antiarthritic,  
 CC antiangiogenic, antiapoptotic and endocrine activities. An antibody (IX)  
 CC specific for an epitope of (I) is useful for inhibiting tumour growth or  
 CC angiogenesis in a subject. (I), a DS fusion polypeptide (III) or a dimeric  
 CC or trimeric fusion polypeptide (III) can be used for inhibiting EC  
 CC migration, proliferation, invasion, or angiogenesis, or for inducing EC  
 CC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X)  
 CC comprising (I), (II), or (III), can be used for treating a subject having  
 CC a disease or condition associated with undesired EC migration,  
 CC proliferation, invasion or angiogenesis. (I), (II), or (III) can be used  
 CC for isolating a DS domain binding molecule from a complex mixture and for  
 CC isolating or enriching cells expressing DS domain binding sites from a  
 CC cell mixture. The present sequence represents the mature human high  
 CC molecular weight kininogen (HK) protein, which is given in the  
 CC exemplification of the present invention  
 XX Sequence 626 AA:  
 SQ Query Match 90.0%; Score 618; DB 5; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GRDFVQPTKICVGCPDPTNSPELTLTTITLNAAENNATYFKIDNVKARVQVV 62  
 Db 235 GRDFVQPTKICVGCPDPTNSPELTLTTITLNAAENNATYFKIDNVKARVQVV 294  
 Qy 63 AGKCKYFIDFVARETCSKESNELTESETKLGQSUDCNAEVYVPMKCKYPT 118  
 Db 295 AGKCKYFIDFVARETCSKESNELTESETKLGQSUDCNAEVYVPMKCKYPT 350  
 RESULT 11  
 ID ABG21101 Standard; protein: 644 AA.  
 XX AC ABG21101;  
 XX DT 18-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #41092.  
 KW Human; chromosome mapping; Gene mapping; Gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.

XX PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PP 30-MAR-2001; 2001WO-US008631.  
 XX PR 31-MAR-2000; 2000US-00540217.  
 XX PR 23-AUG-2000; 2000US-00649167.  
 XX PA (HYSB-) HYBBQ INC.  
 XX PI Dumanac RT, Liu C, Tang YT,  
 XX DR WPI; 2001-639362/73.  
 XX DR N-FSDB; AAS65288.  
 XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX PS Claim 20; SEQ ID NO 51460; 103pp; English.  
 XX PS The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (II) is useful in gene therapy techniques to restore normal  
 CC activity of (III) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue as molecular weight markers and as a food  
 CC supplement. (II), and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensic, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic  
 CC patent did not appear in the printed specification. Note: The sequence data for this  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 644 AA:  
 Query Match 90.0%; Score 618; DB 4; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy - 3 GRDFVQPTKICVGCPDPTNSPELTLTTITLNAAENNATYFKIDNVKARVQVV 62  
 Db 253 GRDFVQPTKICVGCPDPTNSPELTLTTITLNAAENNATYFKIDNVKARVQVV 312  
 Qy 63 AGKCKYFIDFVARETCSKESNELTESETKLGQSUDCNAEVYVPMKCKYPT 118  
 Db 313 AGKCKYFIDFVARETCSKESNELTESETKLGQSUDCNAEVYVPMKCKYPT 368  
 RESULT 12  
 ID ABB78710  
 ID ABB78710 standard; protein: 644 AA.  
 XX AC ABB78710;  
 XX DT 18-JUL-2002 (first entry)  
 DE Human high molecular weight kininogen (HK) protein.  
 KW Human; kininogen; high molecular weight kininogen; HK; DS domain/  
 KW DS receptor; angiogenesis; endothelial cell; cytostatic; antitumour /  
 OS Homo sapiens.

KW antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic;  
 KW ophthalmological; gynaecological; antihyperlipidaemic; antiarrhythmic;  
 KW antiangiogenic; anticlotting; antidiabetic; antihypertensive; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 KEY Location/Qualifiers  
 PT 1..18  
 PT /label= signal  
 PT Protein  
 PT 19..644 /label= mature\_human\_high\_molecular\_weight\_kininogen  
 PT Dsulfide-bond 28..614  
 PT Dsulfide-bond 9..94  
 PT Dsulfide-bond 107..126  
 PT Dsulfide-bond 142..145  
 PT Dsulfide-bond 206..218  
 PT Dsulfide-bond 229..248  
 PT Dsulfide-bond 264..267  
 PT Dsulfide-bond 328..340  
 PT Dsulfide-bond 351..370  
 PT Domain 402..526  
 PT /label= D5\_domain  
 XX  
 PN WO200214369-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PP 24-JUL-2001; 2001WO-US0202185.  
 PR 24-JUL-2000; 2000US-0220194P.  
 XX  
 PA (ATEB-) ATTENON LLC.  
 XX  
 PI Mazar AP, Juarez JC,  
 XX DR WPI, 2002-3361/42.  
 XX  
 PT Novel human kininogen D5 domain polypeptides useful for treating  
 PT conditions associated with endothelial cell migration, proliferation,  
 PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign  
 PT hyperplasia.  
 XX  
 PS Disclosure: Fig 1B-E; BPP: English.  
 XX  
 CC The present invention describes an isolated polypeptide (I) that  
 CC corresponds to the D5 domain of human kininogen, or biologically active  
 CC peptide fragment, homologue or functional derivative, and which: (a)  
 CC inhibits angiogenesis; (b) binds to the D5 binding site on endothelial  
 CC cell (EC); (c) activates signalling pathways leading to the introduction  
 CC of apoptosis in EC; and/or (d) inhibits the signalling pathway required  
 CC for maintenance of EC, and/or (e) inhibits the signalling pathway required  
 CC for maintaining EC, antitumour, (I) has cyclostatic, antitumour,  
 CC antiatherosclerotic, vasotropic, vulnerary, tranquilliser, thrombolytic,  
 CC ophthalmological, gynaecological, anticlotting, antihypertensive,  
 CC antiangiogenic, antidiabetic, antihyperlipidaemic, antiarrhythmic,  
 CC specific for an epitope of (I) or a dimeric fusion polypeptide (II) or a dimeric  
 CC or trimeric fusion polypeptide (III) can be used for inhibiting EC  
 CC migration, proliferation, invasion, or angiogenesis, or for inducing EC  
 CC apoptosis. An angiogenic EC-targeted pharmaceutical composition (X)  
 CC comprising (I), (II), or (III), can be used for treating a subject having  
 CC a disease or condition associated with undesired EC migration,  
 CC proliferation, invasion or angiogenesis. (I), (II), or (III) can be used  
 CC for isolating a D5 domain binding molecule from a complex mixture and for  
 CC isolating or enriching cells expressing D5 domain binding sites from a  
 CC cell mixture. The present sequence represents the human high molecular  
 CC weight kininogen (HK) protein, which is given in the exemplification of  
 XX the present invention  
 SQ sequence 644 AA;

Query Match 90.0%; Score 618; DB 5; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 5..62/  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PT

KW	3 GKDFFQPPTKICVGGCPDIFTNSPELRETLLTITKNAENNATYFKIDNVKKKARRVQVV	62
KW	253 GKDFFQPPTKICVGGCPDIFTNSPELRETLLTITKNAENNATYFKIDNVKKKARRVQVV	312
FH	63 AGKXKFIDFVARETCSKSNEELTESCTKLGQSCLDNCAEVYYPWEKKIYPTV	118
PT	313 AGKXKFIDFVARETCSKSNEELTESCTKLGQSCLDNCAEVYYPWEKKIYPTV	368
PT	RESULT 13	
PT	ABU99150	
PT	ID ABU99150 standard; protein; 644 AA.	
PT	XX	
PT	AC ABU99150/	
PT	XX	
PT	XX	
PT	01-AUG-2003 (first entry)	
PT	DB Novel human GPCR related protein Nov12h.	
PT	XX	
PT	Human, G-protein coupled receptor related protein; GPCR related protein;	
PT	KW NOV; cyclostatic; cardiotonic; antiarteriosclerotic; anti-diabetic;	
PT	KW immunomodulator; anti-HIV; anorectic; antiarrheal; haemostatic;	
PT	KW anti-parkinsonian; neuroprotective; nootropic; gene therapy; vaccine;	
PT	KW NOVX-associated disorder; cardiomyopathy; thromboclerosis; cancer;	
PT	KW diabetes; immune disorder; AIDS; obesity; asthma;	
PT	KW hematopoietic disorder; Parkinson's disease; Alzheimer's disease;	
PT	KW infection; multiple sclerosis; cancer-associated cachexia;	
PT	KW wasting disorder; chronic disease; neurogenesis; cell differentiation;	
PT	KW cell proliferation; haemoptysis; wound healing; angiogenesis;	
PT	KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.	
PT	XX	
PT	OS Homo sapiens.	
PT	XX	
PT	PN WO200214369-A2.	
PT	XX	
PT	PD 12-DEC-2002.	
PT	XX	
PT	PP 04-JUN-2002; 2002WO-US017428.	
PT	XX	
PT	PR 04-JUN-2001; 2001US-0295607P.	
PT	PR 04-JUN-2001; 2001US-0295661P.	
PT	PR 06-JUN-2001; 2001US-0295404P.	
PT	PR 06-JUN-2001; 2001US-0295418P.	
PT	PR 06-JUN-2001; 2001US-0295556P.	
PT	PR 21-JUN-2001; 2001US-0295949P.	
PT	PR 26-JUN-2001; 2001US-0100883P.	
PT	PR 28-JUN-2001; 2001US-0311550P.	
PT	PR 13-AUG-2001; 2001US-0311972P.	
PT	PR 27-AUG-2001; 2001US-0315071P.	
PT	PR 29-AUG-2001; 2001US-0315266P.	
PT	PR 14-SEP-2001; 2001US-0312293P.	
PT	PR 17-SEP-2001; 2001US-0312706P.	
PT	PR 14-DEC-2001; 2001US-031186P.	
PT	PR 28-FEB-2002; 2002US-0316189P.	
PT	PR 12-MAR-2002; 2002US-031671P.	
PT	PR 12-MAR-2002; 2002US-031676P.	
PT	PR 03-JUN-2002; 2002US-00363676.	
PT	XX	
PT	(CURA-) CURAGEN CORP.	
PT	XX	
PT	Anderson DM, Baumgartner JC, Boldog PL, Casman SW, Edinger SR,	
PT	Gierach VL, Gorman L, Guo X, Hjalt T, Kekida R, Li L;	
PT	Maddongall JR, Malyankar UM, Miller J, Padigaru M, Paturajan M,	
PT	Perry CA, Raschell J, Shimkets RA, Stone DJ, Spytek RA,	
PT	Vernet CAM, Voss EZ, Zarhusen BD,	
PT	XX	
PT	DR WO: 2003-140577/13.	
PT	DR N-PSDB; ACD0354.	
PT	New NOVX polypeptides and nucleic acids, useful for preventing or PT treating NOVX-associated disorders, e.g. cancer, cardionopathy,	

Sequence 644 AA:

Sequence	Start	End	Score	Length	DB	Length
Query	0	100	90.0%	90.0%	Score 618;	Length 644;
Match	0	100	100.0%	100.0%	Pred. No. 5	Length 62;
Local Similarity	0	100	5.5e-62	5.5e-62	Conservative	Indels
Best Local Matches	0	100	0	0	Mismatches	0;
Matches	0	100	116	116	Deletions	0;
Consecutive	0	100	0	0	Insertions	0;
3	253	333	GKDfVQPPTKICVGCPDIPNSPELETITHTKNAENDNATPYKIDN	80	GKDfVQPPTKICVGCPDIPNSPELETITHTKNAENDNATPYKIDN	80
253	333	63	AGKKYFIDEVARETTCKAKSNRBLTESCETKKGQSLDNCNAEVVVYPWEEK	80	AGKKYFIDEVARETTCKAKSNRBLTESCETKKGQSLDNCNAEVVVYPWEEK	80

ISU0114  
U93145 ABU99145 standard; protein; 644 AA.

卷之三

0399145;

1-AUG-2003 (first entry)

卷之三

3861 Human Celiac Disease Proteinase.

human; G-protein coupled receptor related

DV, cytosatic, cardiant / antiarteriosclerotic

anti-HIV; anorectic; no effect on parkinsonian; neuroleptic

СССР - вважається діючим дипломатичним представництвом України в Ізраїлі.

Diabetes; immune disorder; AIDS; obesity;

**Amphotericin B** (Fungizone) is a cyclic polyene antibiotic.

neurodegenerating disorder / chronic disease /

cell proliferation; haemopoiesis; wound

chromosome mapping; to review typing; prevent

COMO SAPERE.

200299116-A2.

3 - DEC - 2002.

4-JUN-2002; 2002WO-US017428.

04-JUN-2001	2001US-0295607P.
04-JUN-2001	2001US-0296461P.
06-JUN-2001	2001US-0296404P.
06-JUN-2001	2001US-0296418P.
14-JUN-2001	2001US-0298259P.
15-JUN-2001	2001US-0298555P.
21-JUN-2001	2001US-0299949P.
26-JUN-2001	2001US-0300884P.
28-JUN-2001	2001US-0301550P.
13-AUG-2001	2001US-0311974P.
27-AUG-2001	2001US-0315071P.
29-AUG-2001	2001US-0316650P.
14-SEP-2001	2001US-0322293P.
17-SEP-2001	2001US-0322706P.
14-DEC-2001	2001US-0341186P.
28-FEB-2002	2002US-0346118P.
12-MAR-2002	2002US-0363674P.
12-MAR-2002	2002US-036378P.
03-MAR-2002	2002US-0363676.

New NO<sub>X</sub> polypeptides and nucleic acids, useful for preventing or treating NO<sub>X</sub>-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or pharmacogenomics.

The invention describes an isolated polypeptide (I) comprising any of 27 118-961 residue amino acid sequences, given in the specification, a mature form of them, a sequence that is at least 95% identical to them, or a sequence having one or more conservative substitutions in them. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease selected from a pathology associated with the polypeptide. The NOX polypeptides, poly nucleotides and antibodies are useful in treating or preventing NOX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's disease, Alzheimer's disease, infections, multiple sclerosis, cancer-associated cachexia, and other wasting disorders associated with chronic diseases. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haemato poiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOX substances for use in therapeutic or diagnostic method. The nucleic acids are further used as hybridisation probes in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This is the amino acid sequence of a novel human G-protein coupled receptor related protein NOV.

CX	Sequence 644 AA:	CX	Sequence 644 AA:
Q		Q	
Query Match	90.0%; Score 618; DB 6; Length 644;	Query Match	90.0%; Score 618; DB 6; Length 644;
Best Local Similarity	100.0%; Prod. No. 5 5e-62;	Best Local Similarity	100.0%; Prod. No. 5 5e-62;
Matches	116;	Mismatches	0;
Conservative	0;	Indels	0;
Matches	116;	Gaps	0;
Dy		Dy	
3	GKFRQPFPTKICVGPDRDPTNSPLEETLTHITKINAAENNATYFKIDDNVKKKRQVV	3	GKFRQPFPTKICVGPDRDPTNSPLEETLTHITKINAAENNATYFKIDDNVKKKRQVV
253	GKDFVQPFPTKICVGPDRDPTNSPLEETLTHITKINABNNATYFKIDDNVKKKRQVV	253	GKDFVQPFPTKICVGPDRDPTNSPLEETLTHITKINABNNATYFKIDDNVKKKRQVV
Dy		Dy	
63	AGKYYFDIDFVAREFTTCSKEENEETTSCTKKLGQSIDCNAEVYYVWEEKIYPP	63	AGKYYFDIDFVAREFTTCSKEENEETTSCTKKLGQSIDCNAEVYYVWEEKIYPP

Db 313 AGKCKYIDPVARETTCSKESEELTESETKKIGQSLDCNAEVVYPWEEKIVPTV 368

RESULT 15

AAB37447  
ID AAB37447 standard; protein; 122 AA.  
XX  
AC AAB37447/  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DB Human kininogen D3.  
XX  
KW Enzyme; legumain; endopeptidase; cystatin; human; kininogen.  
XX  
OS Homo sapiens.  
XX  
PN WO200065945-A1.  
XX  
PD 02-NOV-2000.  
XX  
PP 20-APR-2000; 2000WO-GB001571.  
XX  
PR 22-APR-1999; 99GB-00009133.  
XX  
(BABR-) BABRAHAM INST.  
XX  
PA  
XX  
PI Abrahamsen M., Barrett AJ;  
XX  
DR 2000-67316/67.  
XX  
PT Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of cystatin.  
XX  
PS Disclosure: Fig 4: 45pp; English.  
XX  
CC The present invention relates to inhibition of the enzymatic activity of legumain or a legumain-related endopeptidase by cystatin. The inhibition CC involves an interaction between legumain and a papain-non-reactive site CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and CC performs a protein-processing function. The present sequence is human CC kininogen D3, which was used in the present invention. Kininogen is a CC type 3 cystatin  
XX  
SQ Sequence 122 AA;

Query Match 85.3%; Score 586; DB 3; Length 122;  
Best Local Similarity 100.0%; Prod. No. 2.7e-59;  
Matches 110; Conservative 0; N matches 0; Indels 0; Gaps 0;

Qy 9 PPVKICVGCPDIPNSPELEBTHTITKMAENNATPFKIDNPKARVQVAGKYP 68  
1 PPVKICVGCPDIPNSPELEBTHTITKMAENNATPFKIDNPKARVQVAGKYP 60

Qy 69 IDPVARETTCSKESEELTESETKKIGQSLDCNAEVVYPWEEKIVPTV 118  
Db 61 IDPVARETTCSKESEELTESETKKIGQSLDCNAEVVYPWEEKIVPTV 110

GenCore version 5.1.6  
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## OM protein search, using SW model

Run on: September 24, 2004, 14:07:01 {Search time 14.732 Seconds}

(without alignments)  
445.051 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDPYQPPTRKICVGCPRD.....VPWEKKIYPPTVNHWECEF 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgnt\_6/prodata/2/iaa/5A COMB.pep:  
2: /cgnt\_6/prodata/2/iaa/5B COMB.pep:  
3: /cgnt\_6/prodata/2/iaa/5A-COMB.pep:  
4: /cgnt\_6/prodata/2/iaa/6A-COMB.pep:  
5: /cgnt\_6/prodata/2/iaa/6B-COMB.pep:  
6: /cgnt\_6/prodata/2/iaa/bactfisi1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	558	81.2	117	1	US-08-193-111B-1	Sequence 1, Appli
2	556.5	81.0	117	5	PCT-US92-0680-1	Sequence 1, Appli
3	163.5	23.8	145	2	US-08-832-535-2	Sequence 2, Appli
4	163.5	23.8	145	3	US-09-019-485-2	Sequence 2, Appli
5	163.5	23.8	145	3	US-09-019-485-3	Sequence 3, Appli
6	163.5	23.8	145	3	US-09-043-480-9	Sequence 9, Appli
7	163.5	23.8	145	3	US-09-617-302-9	Sequence 9, Appli
8	163.5	23.8	145	4	US-09-528-436B-2	Sequence 2, Appli
9	163	23.7	178	2	US-08-791-522-1	Sequence 1, Appli
10	163	23.7	178	3	US-09-314-777-1	Sequence 1, Appli
11	138.5	20.2	121	4	US-09-775-932-14	Sequence 14, Appli
12	138.5	20.2	128	4	US-09-775-932-12	Sequence 12, Appli
13	138.5	20.2	149	2	US-08-461-030-2	Sequence 2, Appli
14	138.5	20.2	149	3	US-08-744-138-2	Sequence 2, Appli
15	138.5	20.2	149	3	US-09-431-480-8	Sequence 8, Appli
16	138.5	20.2	149	3	US-09-431-480-10	Sequence 10, Appli
17	138.5	20.2	149	3	US-09-617-302-8	Sequence 8, Appli
18	138.5	20.2	149	3	US-09-517-302-10	Sequence 10, Appli
19	138.5	20.2	149	4	US-09-241-376-12	Sequence 2, Appli
20	138.5	20.2	149	4	US-09-940-497-2	Sequence 2, Appli
21	137.5	20.0	112	4	US-08-849-303-16	Sequence 16, Appli
22	136.5	19.9	118	4	US-09-775-932-24	Sequence 24, Appli
23	135.5	19.7	146	6	543264-6	Patent No. 543264
24	134	19.5	148	5	PCT-US95-07158-2	Sequence 2, Appli
25	132.5	19.3	120	4	US-09-775-932-12	Sequence 11, Appli
26	132.5	19.3	145	2	US-08-832-535-11	Sequence 3, Appli
27	132.5	19.3	146	2	US-08-791-522-3	Sequence 26, Appli

Sequence 3, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 47, Appli  
Sequence 37, Appli  
Sequence 17, Appli  
Sequence 9, Appli  
Sequence 15, Appli  
Sequence 93, Appli  
Sequence 19, Appli  
Sequence 46, Appli  
Sequence 48, Appli  
Sequence 26, Appli

RESULT 1  
US-08-193-111B-1  
Sequence 1, Application US/08193114B  
Patient No. 5473945  
GENERAL INFORMATION:  
APPLICANT: Schmaier, Alvin H.  
ADDRESS: 1000 Two Penn Center Plaza  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/193-114B  
PILING DATE: 9 February 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Application  
APPLICATION NUMBER: Serial No. 5472945 07/744,545  
PILING DATE: 13 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-137 CI1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3383  
TELEFAX: (215) 568-5549  
TELEX: No. 5472945E  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: Peptide  
TOPOLOGY: linear  
US-08-193-111B-1

Query Match Score: 81.2%; Score 558; DB 1; Length 117;  
Best Local Similarity 100.0%; Prod. No. 2.3e-55;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CGCPRDIPNSPELBETLTHITKLAENNATYPKIDNYKARVQVAGCKYFDFVA 73  
 Db 1 CGCPRDIPNSPELBETLTHITKLAENNATYPKIDNYKARVQVAGCKYFDFVA 60

Qy 74 RETTCSKESNEBUTESCETKLGSQSDCHAEVTVPWERCKYPTV 118  
 Db 61 RETTCSKESNEBUTESCETKLGSQSDCHAEVTVPWERCKYPTV 105

RESULT 2  
 PCT-US92-06809-1  
 Sequence 1, Application PC/TUS9206809  
 GENERAL INFORMATION:  
 APPLICANT: Schmaier, Alvin H.  
 TITLE OF INVENTION: Modulation of Blood  
 Type of Invention: Process by Altering Bradykinin Levels  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Temple University - Of the  
 ADDRESS: A Commonwealth System of Higher Education  
 STREET: 416 University Services  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06809  
 FILING DATE: 19910813  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. Application  
 APPLICATION NUMBER: Serial No. 744,545  
 FILING DATE: 13 August 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monaco, Daniel A.  
 REGISTRATION NUMBER: 30,480  
 REFERENCE/DOCKET NUMBER: 6056-137  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-5383  
 TELEX: (215) 568-5549  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 PCT-US92-06809-1

Query Match Score 556.5; DB 5; Length 117;  
 Best Local Similarity 93.8%; Pred. No. 3.3e-55; Indels 5; Gaps 1;  
 Matches 106; Conservative 1; Mismatches 1;

Qy 14 CGCPRDIPNSPELBETLTHITKLAENNATYPKIDNYKARVQVAGCKYFDFVA 73  
 Db 1 CGCPRDIPNSPELBETLTHITKLAENNATYPKIDNYKARVQVAGCKYFDFVA 60

Qy 74 RETTCSKESNEBUTESCETKLGSQSDCHAEVTVPWERCKYPTV 118  
 Db 61 RETTCSKESNEBUTESCETKLGSQSDCHAEVTVPWERCKYPTV---NCE 108

GENERAL INFORMATION:  
 APPLICANT: Li, Haodong  
 APPLICANT: Wu, Guo-Liang  
 APPLICANT: Gentz, Rainer  
 TITLE OF INVENTION: HUMAN CYSTATIN P  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/032,535  
 FILING DATE: 03-APR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KIMBALL, PAUL C.  
 REGISTRATION NUMBER: 34,610  
 REFERENCE/DOCKET NUMBER: PP265  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 994-1700  
 TELEX: (201) 994-1700  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-032,535-2

Query Match Score 163.5; DB 2; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.4e-11; Indels 13; Gaps 3;  
 Matches 37; Conservative 22; Mismatches 45;

Qy 11 TKICVGCPGRDIPNTNPELBETLTHITKLAENNATYPKIDNYKARVQVAGCKYFID 70  
 :::  
 Db 32 SRVKGPGPKTKTNQDGQARYSVEKFNNCTNDMPLKESRTRALVQVGLKMLE 91.

Qy 71 FVARETCGSKESNEBUTESCET---TKKLGQSLDCNABVTVWPWERCKYPTV 124  
 :::  
 Db 92 VZGRTTCKQHQL-DCDFTQHFLKQTSCTSEWVWPM-----LQHFE 138

RESULT 4  
 US-08-019-485-2  
 Sequence 2, Application US/09019485  
 GENERAL INFORMATION:  
 APPLICANT: Li, Haodong  
 APPLICANT: Wu, Guo-Liang  
 APPLICANT: Gentz, Rainer  
 APPLICANT: Ni, Jian  
 TITLE OF INVENTION: Cystatin F  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: US  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 3  
 US-08-032-515-2  
 Sequence 2, Application US/08832535  
 Patent No. 5919658

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/019,485  
 PILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Benson, Robert H.  
 REGISTRATION NUMBER: 30,446  
 REFERENCE/DOCKET NUMBER: PP265P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 3013098504  
 TELEX/FAX: 3013098439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-019-485-2

Query Match 23.8%; Score 163.5; DB 3; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
 Mismatches 45; Indels 13; Gaps 3;  
 Matches 37; Conservative 22;

Qy 11 TKICVGCPDRDPTNSPELETITLTKLNANNAATPYFKIDNPKYRQVVAAGKXPFID 70  
 Db 32 SRVXPGPPTKIKNDPGVLQAAARSYEKPNNTCDNMFLFESRTRALVQIVKGKLYMLE 91

Qy 71 FVARETTCSEKSENELTESE--TKKLGQSUDCNEAVYYVPWHRKIYPTVTNHWE 124  
 Db 92 VEGRTTCKQNHLRL-DDCDFQTNTLKTQTLSCYSSEVVTPW-----LQHPE 138

RESULT 5  
 US-09-019-485-3  
 Sequence 3, Application US/09019485  
 Patent No. 6086617  
 GENERAL INFORMATION:  
 APPLICANT: Li, Haodong  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Genz, Reiner  
 APPLICANT: Ni, Jian  
 TITLE OF INVENTION: Cystatin F  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 ZIP: 20850  
 COUNTRY: US

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/019,485  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Benson, Robert H.  
 REGISTRATION NUMBER: 30,446  
 REFERENCE/DOCKET NUMBER: PP265P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 3013098504  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-09-019-485-3  
 Query Match 23.8%; Score 163.5; DB 3; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
 Mismatches 45; Indels 13; Gaps 3;  
 Matches 37; Conservative 22;

Qy 11 TKICVGCPDRDPTNSPELETITLTKLNANNAATPYFKIDNPKYRQVVAAGKXPFID 70  
 Db 32 SRVXPGPPTKIKNDPGVLQAAARSYEKPNNTCDNMFLFESRTRALVQIVKGKLYMLE 91

Qy 71 FVARETTCSEKSENELTESE--TKKLGQSUDCNEAVYYVPWHRKIYPTVTNHWE 124  
 Db 92 VEGRTTCKQNHLRL-DDCDFQTNTLKTQTLSCYSSEVVTPW-----LQHPE 138

RESULT 6  
 US-09-431-480-9  
 Sequence 9, Application US/09431480  
 GENERAL INFORMATION:  
 APPLICANT: Hollaway, James L.  
 APPLICANT: Padhaus, Andrew  
 TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T  
 FILE REFERENCE: 98-72  
 CURRENT APPLICATION NUMBER: US/09/431,480  
 CURRENT FILING DATE: 1999-11-01  
 EARLIER APPLICATION NUMBER: 60/109,217  
 EARLIER FILING DATE: 1998-11-20  
 EARLIER APPLICATION NUMBER: 60/156,382  
 EARLIER FILING DATE: 1999-09-28  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 9  
 LENGTH: 145  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-431-480-9

Query Match 23.8%; Score 163.5; DB 3; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
 Mismatches 45; Indels 13; Gaps 3;

Qy 11 TKICVGCPDRDPTNSPELETITLTKLNANNAATPYFKIDNPKYRQVVAAGKXPFID 70  
 Db 32 SRVXPGPPTKIKNDPGVLQAAARSYEKPNNTCDNMFLFESRTRALVQIVKGKLYMLE 91

Qy 71 FVARETTCSEKSENELTESE--TKKLGQSUDCNEAVYYVPWHRKIYPTVTNHWE 124  
 Db 92 VEGRTTCKQNHLRL-DDCDFQTNTLKTQTLSCYSSEVVTPW-----LQHPE 138

RESULT 7  
 US-09-617-302-9  
 Sequence 9, Application US/09617302  
 Patent No. 6245529  
 GENERAL INFORMATION:  
 APPLICANT: Hollaway, James L.  
 APPLICANT: Padhaus, Andrew  
 TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T  
 FILE REFERENCE: 98-72 C1  
 CURRENT APPLICATION NUMBER: US/09/617,302  
 CURRENT FILING DATE: 2000-07-17  
 PRIOR APPLICATION NUMBER: 09/431,480  
 PRIOR FILING DATE: 1999-11-01  
 PRIOR APPLICATION NUMBER: 60/109,217  
 PRIOR FILING DATE: 1998-11-20  
 PRIOR APPLICATION NUMBER: 60/156,382  
 PRIOR FILING DATE: 1999-09-28  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 9  
 LENGTH: 145

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-617-302-9

Query Match 23.8%; Score 163.5; DB 3; Length 145;  
Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

Qy 11 TKICVGCPDRDIPNSPLEELTHTITKLNAAENNATYFKIDNVKARYVAGKXKPID 70  
Db 32 SRVKPGFPKTKNDPQLQARYSVEFNCTNDMPLFKESRITRALQIVGLKMLB 91

Qy 71 FVARETCSCSNEBELTESC -- -TKKLGQSLSDNAAENATYFWKCKIYPTVTVNHW 124  
Db 92 VEIGRTCKXKQURL-DDCDPFQTNHKLQTLSCYSEWWVPW-----LQHFE 138

RESULT 8  
US-09-528-436B-2  
Sequence 2, Application US/09528436B  
Patent No. 6576745  
GENERAL INFORMATION:  
APPLICANT: Li, et al.  
TITLE OF INVENTION: Human Cystatin P  
FILE REFERENCE: PF265P1D1  
CURRENT APPLICATION NUMBER: US/09/528,436B  
CURRENT FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 09/019,495  
PRIOR FILING DATE: 1998-01-29  
PRIOR APPLICATION NUMBER: 08/832,535  
PRIOR FILING DATE: 1999-04-03  
PRIOR APPLICATION NUMBER: 60/014,795  
PRIOR FILING DATE: 1996-04-03  
NUMBER OF SEQ ID NOS: 16  
SEQ ID NO 2  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-528-436B-2

Query Match 23.8%; Score 163.5; DB 4; Length 145;  
Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

Qy 11 TKICVGCPDRDIPNSPLEELTHTITKLNAAENNATYFKIDNVKARYVAGKXKPID 70  
Db 32 SRVKPGFPKTKNDPQLQARYSVEFNCTNDMPLFKESRITRALQIVGLKMLB 91

Qy 71 FVARETCSCSNEBELTESC -- -TKKLGQSLSDNAAENATYFWKCKIYPTVTVNHW 124  
Db 92 VEIGRTCKXKQURL-DDCDPFQTNHKLQTLSCYSEWWVPW-----LQHFE 138

RESULT 9  
US-09-791-522-1  
Sequence 1, Application US/08791522  
Patent No. S933817  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
TITLE OF INVENTION: Novel Human Cystatin-Like  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ZIP: 94304  
COUNTRY: USA

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PasteSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/314,777  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,522  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0193 US

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-845-4055  
 TELEX/FAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
     LENGTH: 178 amino acids  
     TYPE: amino acid  
 STRANDBNESS: single  
 IMMEDIATE SOURCE:  
     CLONE: 31443

RESULT 11  
 US-09-775-932-1:  
 Sequence 14, Application US/09775932

PATENT NO. 6544477  
 GENERAL INFORMATION:  
 APPLICANT: University of British Columbia  
 TITLE OF INVENTION: Production and use of Modified Cystatins  
 FILE REFERENCE: 58069  
 CURRENT APPLICATION NUMBER: US/09775\_932  
 CURRENT FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: CA99/00717  
 PRIOR FILING DATE: 1999-08-05  
 PRIOR APPLICATION NUMBER: 60/095,503  
 PRIOR FILING DATE: 1998-08-05  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 14  
 LENGTH: 121  
 TYPE: PRT  
 ORGANISM: Homo sapiens

RESULT 12  
 US-09-775-932-1:  
 Sequence 12, Application US/09775932  
 PATENT NO. 6544477  
 GENERAL INFORMATION:  
 APPLICANT: University of British Columbia  
 TITLE OF INVENTION: Production and use of Modified Cystatins  
 FILE REFERENCE: 58069  
 CURRENT APPLICATION NUMBER: US/09775\_932  
 CURRENT FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: CA99/00717  
 PRIOR FILING DATE: 1999-08-05

Query Match 20.2%; Score 138.5; DB 4; Length 121;  
 Best Local Similarity 31.5%; Pred. No. 4.9e-08;  
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
 Db 2 PQRMVGBLRDSDPDPQVKAAAVASYNGNSIYPRDTIKAQSQLVAGIKYFL 61  
 Qy 10 PTKICVCPDPTNSPELETHTITKLNAENNATPYFKIDNYKKARVQVYAGIKYFL 69  
 Db 70 DPAARETCSKE---SNEBLTSSCTKLGG---SLDCNAAEVVVPWE 111  
 Qy 62 TMEMGSTDCRKTRVTGHDYDLT-TCPLAGAQEQKRCDFEVLPWQ 108

RESULT 12  
 Sequence 12, Application US/09775932  
 PATENT NO. 6544477  
 GENERAL INFORMATION:  
 APPLICANT: University of British Columbia  
 TITLE OF INVENTION: Production and use of Modified Cystatins  
 FILE REFERENCE: 58069  
 CURRENT APPLICATION NUMBER: US/09775\_932  
 CURRENT FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: CA99/00717  
 PRIOR FILING DATE: 1999-08-05

Query Match 20.2%; Score 138.5; DB 4; Length 128;  
 Best Local Similarity 31.3%; Pred. No. 5.2e-08;  
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
 Db 9 PQRMVGBLRDSDPDPQVKAAAVASYNGNSIYPRDTIKAQSQLVAGIKYFL 68  
 Qy 10 PTKICVCPDPTNSPELETHTITKLNAENNATPYFKIDNYKKARVQVYAGIKYFL 69  
 Db 69 TMEMGSTDCRKTRVTGHDYDLT-TCPLAGAQEQKRCDFEVLPWQ 115  
 Qy 71 PAARETCSKEEELTESE---TKXKGOSTDNCNAEVVVPW 110  
 Db 114 VBIGRTCKRKNQHLRL-DDCDPQTNTLQLUSCTSEWWVPW 155

RESULT 13  
 US-09-461-030C-2  
 Sequence 2, Application US/08461030C  
 PATENT NO. 5984601  
 GENERAL INFORMATION:  
 APPLICANT: Ni, Jian  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Genter, Reiner  
 APPLICANT: Rosen, Craig A.  
 TITLE OF INVENTION: Human Cystatin E  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Ave  
 CITY: Rockville  
 STATE: MD  
 COUNTY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461.030C  
 FILING DATE: 05-JUN-1995  
 CLASIFICATION: 415  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Anders, Brooks  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PP202  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8439  
 TELEX/FAX: 301-309-8439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 149 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 20.2%; Score 138.5; DB 2; Length 149;  
 Best Local Similarity 31.5%; Pred. No. 6.4e-08;  
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
 Db 10 PTKICVCPDPTNSPELETHTITKLNAENNATPYFKIDNYKKARVQVYAGIKYFL 69  
 Qy 30 PQRMVGBLRDSDPDPQVKAAAVASYNGNSIYPRDTIKAQSQLVAGIKYFL 89

Qy 70 DFTARETCSKB---SNELTSCETKLKGQ--SLDCNAEVVVFWE 111  
 Db 90 TMENGSTOCRTRVTGRHDT-TCPPLAAGAOQEKLRCDFPEVLPWQ 136

RESULT 14

Sequence 2, Application US/08744138

GENERAL INFORMATION:

Patent No. 6011012

APPLICANT: Gant, Reiner L.

APPLICANT: Ni, Jian

APPLICANT: Rosen, Craig A.

APPLICANT: Yu Guo-Liang

TITLE OF INVENTION: Human Cystatin E

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9310 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/744,138

FILING DATE:

CLASSIFICATION: 415

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE DOCKET NUMBER: PF2032P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301 309 8504

TELEFAX: 301 309 8512

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 149 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-744-138-2

Query Match 20.2%; Score 138.5; DB 3; Length 149;  
 Best Local Similarity 31.5%; Pred. No. 6.4e-08;  
 Matches 34; Conservative 22; Nismatches 45; Indels 7; Gaps 3;

Qy 10 PTKICVGCPDIPSPLEBLTITLNAENNATPYFKIDNVKARVQVAGKVKFI 69  
 Db 30 PQERMVGLRDSDPDPOVKAADAAVASYNGNSYYFPDTTHIKQSOLVAGKVKFL 89

Qy 70 DFTARETCSKB---SNELTSCETKLKGQ--SLDCNAEVVVFWE 111  
 Db 90 TMENGSTOCRTRVTGRHDT-TCPPLAAGAOQEKLRCDFPEVLPWQ 136

RESULT 15

US-09-431-480-6

Sequence 6, Application US/09431480

Patent No. 623708

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

APPLICANT: Feldhaus, Andrew

TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T

FILE REFERENCE: 90-72

CURRENT FILING DATE: 199-11-01

CURRENT APPLICATION NUMBER: US/09/431,480

EARLIER APPLICATION NUMBER: 60/109,217

EARLIER FILING DATE: 1998-11-20

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 24, 2004, 14:05:18 | Search time 36.576 Seconds  
(without alignment)  
1095.549 Million cell updates/sec

Title: US-10-661-784-3  
Perfect score: 687  
Sequence: 1 GSGKDPVQPPPTKICVGCPRD.....VPWKKYPPVTVNHWECBP 127

Scoring table: BLOSUM62  
Gapext 0.5  
Gap 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%  
Listing first 45 summaries

Database : SPREMBL\_25\_\*

1: SP\_archaea:  
2: SP\_bacteria:  
3: SP\_fungi:  
4: SP\_humani:  
5: SP\_invertebrate:  
6: SP\_mammal:  
7: SP\_mhc:  
8: SP\_organelle:  
9: SP\_phage:  
10: SP\_plant:  
11: SP\_rordan:  
12: SP\_virus:  
13: SP\_vertbrate:  
14: SP\_unclassified:  
15: SP\_virus:  
16: SP\_bacteriap:  
17: SP\_archaeap:

RESULTS

No.	Score	Match	Length	DB	ID	Description
1	383	55.7	140	6	Q7YRP6	Q7yyp6 sus scrofa
2	381	55.5	423	11	P70517	P70517 rattus norvegicus
3	378	55.0	430	11	063181	063181 mus musculus
4	171.5	25.0	187	11	Q9NHS5	Q7zj8 homo sapiens
5	163.5	23.8	167	4	Q72438	Q7y91 xenopus laevis
6	152.5	22.2	462	13	Q72791	Q801es xenopus laevis
7	152.5	22.2	462	13	Q76YH2	Q8px9 mus musculus
8	152.5	22.2	465	13	Q801ES	Q8018B brachydanio
9	131.5	19.1	140	11	Q9EPX9	Q8ab17 mus musculus
10	123.5	18.0	455	13	Q80088	Q80125 cyprinus carpio
11	119	17.3	388	11	Q8CB17	Q9nb95 litomosoides
12	117.5	17.1	464	13	Q80125	Q83397 mus musculus
13	113.5	16.5	148	5	Q9NH05	Q80125 cyprinus carpio
14	113	16.4	140	11	Q80Y72	Q9d1b1 mus musculus
15	111	16.2	146	11	Q8K397	Q8018B brachydanio
16	111	16.2	149	11	Q9D1B1	Q80125 cyprinus carpio

ALIGNMENTS

Query	Match	Length	DB	ID	Description
Q7YRP6	55.7%	Score 383; DB 6; Length 140;			
AC	Q7YRP6,	Preliminary;	PRTI	140 AA.	
DT	01-OCT-2003	(TREMBLrel 25; Created)			
DT	01-OCT-2003	(TREMBLrel 25; Last sequence update)			
DT	01-OCT-2003	(TREMBLrel 25; Last annotation update)			
DR	AJ321363; AAPBB260.1;	Submitted (UN-2003) to the EMBL/GenBank/DBJ databases.			
FT	NON_TER	1			
FT	NON_TER	140	140 AA,	15650 MW;	177837836603P777 CRC64;
FT	SEQUENCE	1	NCBI_TaxID=3823;	RN [1]	
FT	SEQUENCE	1	NCBI_TaxID=3823;	RN [1]	
RA	Vonahme K.A., Fernandes S.C., Ross J.A., Ashworth M.D., DaSilva U.,	Best Local Similarity 78.9%; Pred. No. 2, 8e-30;			
RA	Maloyer J.-R., Geisert R.D.,	Mismatches 5; Indels 0, Gaps 0;			
RT	"Porcine Endometrial and Conceptus Expression of Kininogens and Plasma KNG."				
RL	Submitted (UN-2003) to the EMBL/GenBank/DBJ databases.				
DR	AJ321363; AAPBB260.1;				
FT	NON_TER	1			
FT	NON_TER	140	140 AA,	15650 MW;	177837836603P777 CRC64;

Summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	383	Q7YRP6	sus scrofa	55.7	6	P70517	Q7yyp6 rattus norvegicus
2	381	Q7YRP6	rattus norvegicus	55.5	11	P70517	Q7yyp6 rattus norvegicus
3	378	Q7YRP6	mus musculus	55.0	11	063181	Q7zj8 homo sapiens
4	171.5	Q7YRP6	brachydanio	25.0	11	Q9NHS5	Q7y91 xenopus laevis
5	163.5	Q7YRP6	cyprinus carpio	23.8	167	Q72438	Q801es xenopus laevis
6	152.5	Q7YRP6	litomosoides	22.2	462	Q72791	Q8px9 mus musculus
7	152.5	Q7YRP6	brachydanio	22.2	462	Q76YH2	Q8ab17 mus musculus
8	152.5	Q7YRP6	cyprinus carpio	22.2	465	Q801ES	Q80125 cyprinus carpio
9	131.5	Q7YRP6	litomosoides	19.1	140	Q9EPX9	Q80125 cyprinus carpio
10	123.5	Q7YRP6	brachydanio	18.0	455	Q80088	Q80125 cyprinus carpio
11	119	Q7YRP6	cyprinus carpio	17.3	388	Q8CB17	Q80125 cyprinus carpio
12	117.5	Q7YRP6	litomosoides	17.1	464	Q80125	Q80125 cyprinus carpio
13	113.5	Q7YRP6	cyprinus carpio	16.5	148	Q9NH05	Q80125 cyprinus carpio
14	113	Q7YRP6	litomosoides	16.4	140	Q80Y72	Q80125 cyprinus carpio
15	111	Q7YRP6	brachydanio	16.2	146	Q8K397	Q80125 cyprinus carpio
16	111	Q7YRP6	cyprinus carpio	16.2	149	Q9D1B1	Q80125 cyprinus carpio

RESULT 2

P70517	PRELIMINARY,	PRT;	423 AA.	BA
ID P70517/				RT "Primary structure of a gene encoding rat T-kininogen."
DT 01-PFB-1997 (TREMBLrel. 02, Created)				RL Gene 81:119-128 (1989).
DT 01-PFB-1997 (TREMBLrel. 02, Last annotation update)				DR EMBL; M20090 / AAA42251..1 / JOINED.
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				DR EMBL; M20094 / AAA42251..1 / JOINED.
DE Major acute phase alpha-1 protein precursor (Fragment).				DR EMBL; M20091 / AAA42251..1 / JOINED.
OS Rattus norvegicus (Rat).				DR EMBL; M20085 / AAA42251..1 / JOINED.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.				DR EMBL; M20086 / AAA42251..1 / JOINED.
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Rattus.				DR EMBL; M20087 / AAA42251..1 / JOINED.
OC NCBI_TaxID10116;				DR EMBL; M20088 / AAA42251..1 / JOINED.
RN [1]				DR EMBL; M20089 / AAA42251..1 / JOINED.
RP SEQUENCE FROM N.A.				PIR: S68034 / 568034.
RA Cole T.				PIR: S68035 / 568035.
RA Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.				DR InterPro; IP000089; P-cysteine protease inhibitor activity; IBA.
RL RN [2]				DR InterPro; IP000010; Cystatin.
RP SEQUENCER FROM N.A.				DR Pfam; PP00031; Cystatin.
RX MEDLINE=514311; PubMed=2579444;				DR SMART; SM00043; CY3.
RA Cole T., Ingilis A.S., Nagashima M., Schreiber G.;				DR PROSITE; PS00287; CYSTATIN_2.
RT "Major acute phase alpha-1"-protein in the rat: Structure, molecular cloning, and regulation of mRNA levels.",				DR SQ 430 AA; 47618 MW; 45508DBEF4BDC978C CRC64;
RT Biochem. Biophys. Res. Commun. 126:719-724 (1985).				Query Match Score 55.0%; Best Local Similarity 62.1%; Matches 72; Conservative 13; Mismatches 31; Indels 0; Gaps 0;
RN [3]				DR PROSITE; PS00287; CYSTATIN_2.
RP SEQUENCE FROM N.A.				DR SQ 430 AA; 47618 MW; 45508DBEF4BDC978C CRC64;
RX MEDLINE=85127561; PubMed=2578992;				Query Match Score 55.0%; Best Local Similarity 62.1%; Matches 72; Conservative 13; Mismatches 31; Indels 0; Gaps 0;
RA Cole T., Ingilis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;				DR PROSITE; PS00287; CYSTATIN_2.
RT "Major acute phase alpha-1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.",				DR SQ 430 AA; 47618 MW; 45508DBEF4BDC978C CRC64;
RT PNAS Lett. 1:12:57-61 (1985).				Query Match Score 55.0%; Best Local Similarity 62.1%; Matches 72; Conservative 13; Mismatches 31; Indels 0; Gaps 0;
RL PIR: K02814; AAA41561..1; -.				DR PROSITE; PS00287; CYSTATIN_2.
DR PIR: S68034 / 568034.				DR SMART; SM00043; CY3.
DR GO/GO0004889; P-cysteine protease inhibitor activity; IBA.				DR PROSITE; PS00287; CYSTATIN_2.
DR InterPro; IP000010; Cystatin.				DR SQ 430 AA; 46905 MW; FE88BD198547919 CRC64;
DR InterPro; IP000010; Cystatin.				Query Match Score 55.5%; Best Local Similarity 62.1%; Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
DR SMART; SM00043; CY3.				DR PROSITE; PS00287; CYSTATIN_2.
DR PROSITE; PS00287; CYSTATIN_2.				DR SQ 430 AA; 46905 MW; FE88BD198547919 CRC64;
KW Signal	: 1			Query Match Score 55.5%; Best Local Similarity 62.1%; Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;
PT NON TER	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT SIGNAL	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT CHAIN	: 11			DR PROSITE; PS00287; CYSTATIN_2.
PT CHAIN	: 12			DR PROSITE; PS00287; CYSTATIN_2.
PT CHAIN	: 23			DR PROSITE; PS00287; CYSTATIN_2.
PT CHAIN	: 379			DR PROSITE; PS00287; CYSTATIN_2.
SQ SEQUENCE 423 AA;	46905 MW;			DR PROSITE; PS00287; CYSTATIN_2.
DR SMART; SM00043; CY3.				DR PROSITE; PS00287; CYSTATIN_2.
DR PROSITE; PS00287; CYSTATIN_2.				DR PROSITE; PS00287; CYSTATIN_2.
KW Signal	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT NON TER	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT SIGNAL	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT CHAIN	: 11			DR PROSITE; PS00287; CYSTATIN_2.
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DR SMART; SM00043; CY3.				DR PROSITE; PS00287; CYSTATIN_2.
DR PROSITE; PS00287; CYSTATIN_2.				DR PROSITE; PS00287; CYSTATIN_2.
KW Signal	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT NON TER	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT SIGNAL	: 1			DR PROSITE; PS00287; CYSTATIN_2.
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SQ SEQUENCE 423 AA;	46905 MW;			DR PROSITE; PS00287; CYSTATIN_2.
DR SMART; SM00043; CY3.				DR PROSITE; PS00287; CYSTATIN_2.
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SQ SEQUENCE 423 AA;	46905 MW;			DR PROSITE; PS00287; CYSTATIN_2.
DR SMART; SM00043; CY3.				DR PROSITE; PS00287; CYSTATIN_2.
DR PROSITE; PS00287; CYSTATIN_2.				DR PROSITE; PS00287; CYSTATIN_2.
KW Signal	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT NON TER	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT SIGNAL	: 1			DR PROSITE; PS00287; CYSTATIN_2.
PT				

	RN [1]	RN
	RP	SEQUENCE FROM N.A.
	RC	TISSUE=embryo;
	RA	Klein S., Strauberg R.; Submitted: (JAN-2003) to the EMBL/GenBank/DBJ databases.
	RL	
	DR	EMBL: BC04391; AAH3891; -
	DR	DR GO; GO:0004669; ECYDINE protease inhibitor activity; IBA.
	DR	DR InterPro; IPRO0010; Cystatin.
	DR	DR Pfam; PF00031; cystatin_2.
	DR	DR SMART; SM00043; CY_2.
	DR	DR SEQUENCE 462 AA; 5185 MW; D7BAD339961739FB CRC64;
	SQ	
		Query Match Score 152.5; DB 13; Length 462;
		Best Local Similarity 38.8%; Pred. No. 8.4e-07;
		Mismatches 13; Indels 5; Gaps 2;
		Matches 33; Conservative 34; MisMatches 34; Indels 5; Gaps 2;
		Qy 10 PRKICVGCPRDIPITNSPELETLHT---ITKLNAENNATFYFIDVKKARVQQVAGK 65
	Db	Db 142 PGVLISTCP-DCPTANEETPTTITETADTLARYNKSNNTRFYFIDHTERVRSQWVNGP 200
		Qy 66 KYPIDPARETCSESNEELTEC 90
	Db	Db 201 SYIQFTIKETDMKTQENVVLSC 225
		RESULT 7
	Q7SYXH2	PRELIMINARY, PRT; 462 AA.
	ID	Q7SYXH2
	AC	Q7SYXH2;
	DT	01-OCT-2003 (TRMBLrel. 25, Created)
	DT	01-OCT-2003 (TRMBLrel. 25, Last sequence update)
	DT	01-OCT-2003 (TRMBLrel. 25, Last annotation update)
	DE	Oysterin domain, feline-like protein.
	DS	Xenopus laevis (African Clawed Frog).
	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
	OC	Xenopodinae; Xenopus.
	NCBI_TaxID=3155;	RN [1]
	RP	SEQUENCE FROM N.A.
	RC	TISSUE=ventral midgut;
	RA	Costa R.M.B., Mason J., Lee M., Amaya E., Zorn A.M.;
	RA	"Novel gene expression domains reveal early patterning of the Xenopus endoderm.";
	RT	Submitted: (MAR-2003) to the EMBL/GenBank/DBJ databases.
	RL	DR EMBL: AV260332; AAP22891; -
	SQ	SEQUENCE 462 AA; 5186 MW; 796PP92774CC2721 CRC64;
		Query Match Score 152.5; DB 13; Length 462;
		Best Local Similarity 38.8%; Pred. No. 8.4e-07;
		Mismatches 13; Indels 5; Gaps 2;
		Qy 10 PRKICVGCPRDIPITNSPELETLHT---ITKLNAENNATFYFIDVKKARVQQVAGK 65
	Db	Db 142 PGVLISTCP-DCPTANEETPTTITETADTLARYNKSNNTRFYFIDHTERVRSQWVNGP 200
		Qy 66 KYPIDPARETCSESNEELTEC 90
	Db	Db 201 SYIQFTIKETDMKTQENVVLSC 225
		RESULT 8
	Q801ES	PRELIMINARY, PRT; 465 AA.
	ID	Q801ES
	AC	Q801ES;
	DT	01-JUN-2003 (TRMBLrel. 24, Created)
	DT	01-JUN-2003 (TRMBLrel. 24, Last sequence update)
	DT	01-OCT-2003 (TRMBLrel. 25, Last annotation update)
	DB	Similar to fetuin B.
	OS	Xenopus laevis (African Clawed Frog).
	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
	OC	Xenopodinae; Xenopus.
	NCBI_TaxID=8355;	OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
	OC	Xenopodinae; Xenopus.



DR GO:GO:0000869; P:cytsteine protease inhibitor activity; IEA.

DR InterPro; IPR000010; Cystatin.

DR InterPro; IPR01363; Penguin.

DR Pfam; PF00031; cystatin.

DR SMART; S00043; CY; 2.

DR PROSITE; PS01254; PETUN\_1; 1.

DR PROSITE; PS01255; PETUN\_2; 1.

DR SEQUENCE; 388 AA, 42742 MW, 78CPAD73ABD8D22 CRC64;

Query Match Score 119; DB 11; Length 388; Best Local Similarity 25.9%; Prod. No. 0.015; Matches 30; Conservative 28; Mismatches 52; Indels 6; Gaps 3;

Qy 14 CCGCPDPIPTNSPELEPBLTLTHITLNAENNATYFYKIDVYKXARVOVYAGKVKYFDFVA 73

Db 154 CDDCPSDIDNSPALEATESLAKEFNKSRSKCK - ELYKVTAAMNOVSGPAYVSYLI 212.

Qy 74 RPTTCSKESNEBLTSCYTKLGG - QSLDCHNAAEVVYVPPWKKIPTVTWNHWECEP 127

Db 213 KAPCTK6QASCGLHSOSEPVGTCQSTTVQSSLRHPVLIOPVKEVKVTT--CEP 265

RESULT 12

Q80125 ; PRELIMINARY; PRT; 464 AA.

ID Q80125 ; PRELIMINARY; PRT; 464 AA.

AC Q80125 ; PRELIMINARY; PRT; 464 AA.

DT 01-JUN-2003 ; (TREMBL) 24; Created

DR 01-JUN-2003 ; (TREMBL) 24; Last sequence update

DR 01-OCT-2003 ; (TREMBL) 25; Last annotation update

DB Fetus long form.

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.

OX NCBI Taxid:7962;

RN [1]

RP SEQUENCE FROM N.A.

RA "Bai P., L. Chang G.-D., Huang C.-J./ Purification and cloning of carp fetuin,"; ID "Purification and cloning of carp fetuin,"; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY229965; AR074862; 1.

DR GO:GO:000874; Cimicocubule; IEA.

DR GO:GO:000869; P:cytsteine protease inhibitor activity; IEA.

DR GO:GO:000198; P:microtubule molecule activity; IEA.

DR GO:GO:0001018; P:microtubule-based movement; IEA.

DR InterPro; IPR02453; Beta-tubulin.

DR InterPro; IPR00010; Cystatin.

DR SMART; S00043; CY; 1.

DR PROSITE; PS00228; TUBULIN\_B\_AUTOREG; 1.

DR SEQUENCE; 464 AA, 51698 MW, 7A54F1E44050895 CRC64;

Query Match Score 117.5; DB 13; Length 464; Best Local Similarity 24.8%; Prod. No. 0.025; Matches 32; Conservative 23; Mismatches 59; Indels 15; Gaps 4;

Qy 14 CCGCPDPIPTNSPELEPBLTLTHITLNAENNATYFYKIDVYKXARVO-VVAGKVKYFDFV 72

Db 142 CPPCPGULPLMPKGLESVKTALQKPNESDNIKSYPLMSVGRISTOMNSGGSPPSQFA 201

Qy 73 ARETTCSKESNBBLTSC----ETRKUQSLSLCNAEAVVYVPEKKIPTVTNH-W--- 123

Db 202 IMETNCNPKAQNBSSECKALGEKARYGFCKSTKVGIEBPEVECEIVYBAKNTHPKHP 261

Qy 124 ----ECPP 127

Db 262 AQSRDCKP 270

RESULT 13

O9NH95 PRELIMINARY; PRT; 148 AA.

ID O9NH95 PRELIMINARY; PRT; 148 AA.

AC O9NH95 PRELIMINARY; PRT; 148 AA.

SEQUENCE FROM N.A.  
 RC TISSUE=Testicle;  
 RA Strasbourg R.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC048616; AAH48646.; -;  
 DR GO; GO:0004859; P:cytokeratins protease inhibitor activity; IBA.  
 DR InterPro; IPR000010; Cytokeratin.  
 DR InterPro; IPR003243; Cytokeratin\_C/M.  
 DR Pfam; PF00031; cytokeratin\_1.  
 DR SMART; SM00131; Cytokeratin\_C/M; 1.  
 DR SMART; SM0013; CY; 1.  
 SQ SEQUENCE 140 AA; 16199 MW; 32633B99C4697DA0 CRC64;  
 Sequence 140 AA; 16199 MW; 32633B99C4697DA0 CRC64;

Query Match Score 113; DB 11; Length 140;  
 Best Local Similarity 29.4%; Pred. No. 0.018;  
 Matches 25; Conservative 18; Mismatches 38; Indels 4; Gaps 2;

Ov. 28 LEPLLTITKNAERNATPVKIDDNVKARQVNVAGKPKYDFPARETCSKESNEILT 87  
 Db 44 INSTLHPFIRSTNNASTDITLYOQKLIGOMQMLTTSVRLVYTVKIGRTKCK- -NETKK 101

Ov. 88 ESC -ETKLGOSLDCAEYVPPW 110  
 Db 102 ASPLQSSKLKSLICKSLIYSPW 126

---

RESULT 15

Q8KJ97 PRELIMINARY; PRTR; 146 AA.  
 ID Q8KJ97  
 AC Q8KJ97  
 DT 01-OCT-2002 (TREMBLeRl. 22, Created)  
 DT 01-JUN-2002 (TREMBLeRl. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLeRl. 24, Last annotation update)  
 D2 RIKEN cDNA 111001781 gene (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Neacaea; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Adrenal gland;  
 RA Strasbourg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC027680; AAH27680.; -;  
 DR GO; GO:0004859; P:cytokeratins protease inhibitor activity; IBA.  
 DR InterPro; IPR000010; Cytokeratin.  
 DR Pfam; PF00031; cytokeratin; 1.  
 DR SMART; SM00043; CY; 1.  
 PT NON\_TER  
 SQ SEQUENCE 146 AA; 16180 MW; 9D77BB9A6063A54 CRC64;  
 Sequence 146 AA; 16180 MW; 9D77BB9A6063A54 CRC64;

Query Match Score 111; DB 11; Length 146;  
 Best Local Similarity 30.5%; Pred. No. 0.03;  
 Matches 29; Conservative 18; Mismatches 42; Indels 6; Gaps 4;

Ov. 22 PTNSPERBETHTHTKIDRNNTTFKIDNKARVOVAGKPKYDFVARETCSKE 81  
 Db 40 PRD-PRVQAAQAIAVASTNGSDSFLYPRDTKVIAKYQLVAGIXYLTLDIESTCRKT 98

Ov. 82 --SNEED-TESCETRKLGQ--SLUCNAEVYPWEE 111  
 Db 99 RVGHEMDLTCPLAAGGQORKLRCPNPELSEPMK 133

oring table:	BLOSUM62			
gapop 10.0 , Gapext 0.5				
searched:	141681 seqB, 52070155 residues			
total number of hits satisfying chosen parameters:	141681.			
minimum DB seq length: 0				
maximum DB seq length: 2000000000				
st-processing: Minimum Match 0%	Maximum Match 100%			
Listing First 45 summaries				
Swissprot_42:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
Database :	SUMMARIES			
Query No.	Score	Match Length	DB ID	Description
1	618	90.0	KNG_HUMAN	P0102 homo sapien
2	440	64.0	KOHL_BOVIN	P01046 bos taurus
3	440	64.0	KOHNI_BOVIN	P01044 bos taurus
4	413	60.1	KOHNI_BOVIN	P01047 bos taurus
5	413	60.1	KOHNI_BOVIN	P01045 bos taurus
6	413	60.1	KONG_MOUSE	P08677 mus musculi
7	410	59.7	KONG_RAT	P08934 rattus norv
8	388	56.5	KONTZ RAT	P08932 rattus norv
9	380	55.3	KONTZ RAT	P01048 rattus norv
10	171.5	25.0	CYTF_MOUSE	Q89098 mus musculi
11	163.5	23.8	CYTF_MACMU	P01036 homo sapien
12	138.5	20.2	FETB_HUMAN	Q19032 macaca mulu
13	138.5	20.2	CYTF_HUMAN	Q18818 homo sapien
14	137.5	19.7	CYTC_BOVIN	P01035 bos taurus
15	135	19.7	FETB_RAT	Q9QX79 rattus norv
16	132.5	19.3	CYTC_HUMAN	P01034 homo sapien
17	132.5	19.3	CYTC_SPISC	Q19093 saimiri sci
18	131	19.1	FETB_HUMAN	Q9QXC1 homo sapien
19	130	18.9	CYTC_RAT	P14841 rattus norv
20	129.5	18.9	CYTC_MOUSE	P21460 mus musculi
21	128	18.6	CYT_BETAR	P08935 batis ariet
22	124.5	18.1	CYT_HUMAN	P09228 homo sapien
23	124.5	18.1	CYT_RABBIT	Q97862 oryctolagus cuniculus
24	122.5	17.8	CYT_CONJA	P81061 cornutrix co
25	121.9	17.3	PEPE_MOUSE	Q9QXC1 mus musculi
26	118.5	17.2	CYF_CHICK	P01038 gallus gallus
27	113	16.4	CYNS_RAT	P19313 rattus norv
28	109.5	15.9	CYNS_HUMAN	P201037 homo sapien
29	108.5	15.8	CYNS_HUMAN	P201036 homo sapien
30	107	15.6	CYT_ONCOKV	Q98967 oncorynchus leucophrys
31	105.5	15.4	CYT_ONCOKV	P220765 homo sapien
				RESULT 1
				XKG_HUMAN
				ID P01042 ; P01043 ; STANDARD; PRT; 644 AA.
				AC P01042 ; P01043 ; (Rel. 01, Created)
				DT 21-JUL-1986 (Rel. 33, Last sequence update)
				DT 01-FEB-1996 (Rel. 41, Last annotation update)
				DT 10-OCT-2003 (Rel. 42, Last annotation update)
				DE Kininogen Precursor (Alpha-2-thiool proteinase inhibitor) [ContainIn, Bradykinin].
				GN XKG.
				OS Homo sapiens (Human).
				OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi / Mammalia; Butheria; Primates;
				OX NCBI_TaxID:96066;
				RN SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
				RP TISSUE:Liver;
				RX MEDLINE=85134582; PubMed=2989293;
				RA Takagaki Y., Kitamura N., Nakanishi S.;
				RT "Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight prekininogens. Primary structures of two human Prekininogens.";
				RT RL J. Biol. Chem. 260:8601-8609 (1985).
				[2]
				RP GENB STRUCTURE.
				RX MEDLINE=85123483; PubMed=2989294;
				RA Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakanihi S.;
				RA "Structural organization of the human kininogen gene and a model for its evolution.";
				RT RL J. Biol. Chem. 260:8610-8617 (1985).
				[3]
				RP SEQUENCE OF 1-401 FROM N.A.
				RX MEDLINE=85122621; PubMed=641591;
				RA Okubo I., Kurata K., Takasaki T., Shiokawa H., Sasaki M., "Resolution of a human cDNA for a alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen."
				RT RL Biochemistry 23:5591-5697(1984).
				[4]
				RP SEQUENCE OF 379-644.
				RX MEDLINE=8603070; PubMed=4054110;
				RA Lottspeich F., Kellermann J., Henschien A., Foerster B., "The amino acid sequence of the light chain of human high-molecular-mass Kininogen;"
				RT RL Biochemistry 15:307-314 (1985).
				[5]
				RP SEQUENCE OF 361-369.
				RX MEDLINE=90255622; PubMed=4952632;
				RA Miyata T., Kato H., Iwanaga S. ; "Structural features of plasma kinins and kininogens.";
				RT RL Ped. Proc. 27:52-57(1968).
				[6]
				RP DISULFIDE BONDS.
				RX Miyoshi T., Miyata T., Kato H., Iwanaga S. ; "Influence of bonds in bovine HMW kininogens on their J.V. activity";
				RT RT Ped. Proc. 27:52-57(1968).
				RN Onychocerca



21-JUL-1986 (Rel. 01, Last sequence update)  
 DR 15-MAR-2004 (Rel. 43, Last annotation update)

DE Kininogen, Lmw I precursor (thiol protease inhibitor) [Contains:  
 DE Bradykinin]  
 DS Bos taurus (Bovine).  
 OS Bos taurus  
 OC Bovaryota; Metazoa; Chordata; Craniata; Vertebrata; Bivalvia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.  
 NCBI\_TaxID:9913;

RN [1]  
 RP SOURCE FROM N.A. PubMed=6572010; Asai M., Inayama S., Nakanishi S., Nawa H., Kitamura N., Hirose T., Miyata T., Hashimoto N., Kato H., Hayashida H., Sueyoshi T., Miyata T., Miyata T., Iwanaga S.,  
 RA Primary structures of bovine liver low molecular weight kininogen precursors and their two mannosidases. Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).

RN [2]  
 RP SEQUENCE OF 19-378  
 RX MEDLINE=87137530; PubMed=35462951;  
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.,  
 RA Bovine high molecular weight kininogen. The amino acid sequences, positions of carbohydrate chains and disulfide bridges in the heavy chain portion. J. Biol. Chem. 262:12768-12779 (1987).

RN [3]  
 CC FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2) Lmw-kininogen inhibits the aggregation of thrombocytes; (3) the active peptide kallidin that is released from Lmw-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction, (3B) induction of hypotension, (3C) natriuretic and diuretic (kidney).  
 CC SUBCELLULAR LOCATION: Extracellular.

CC ALTERNATIVE PRODUCTS:  
 Event/Alternative splicing, Namad isoforms=2;  
 Name=LWV\_I;  
 IsoID=PO1046-1; SequenceDisplayed;

CC Name=RHW\_I;  
 IsoID=PO1044-1; SequenceExternal:

CC TISSUE SPECIFICITY: Plasma.  
 CC PTM: Bradykinin is released from kininogen by plasma kallikrein.  
 CC MECOBALANEous: Lmw kininogen is in contrast to Hmw-kininogen not involved in blood clotting.

CC SIMILARITY: Contains 3 cystatin-like domains.

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CC EMBL: V00436; CAA23709\_1; -.  
 DR PIR: A01283; KG801.  
 DR InterPro; IPR00010; Cystatin.  
 DR Pfam; PF00031; cystatin\_3.  
 DR SMART; SM00043; CY\_3.  
 DR PROSITE; PS00287; CYSTATIN\_2.  
 KW Glycoprotein, Plasma; Repeat; Vasodilator; Alternative splicing;  
 KW Thiol protease inhibitor; Bradykinin; Signal; Pyrrolidone carboxylic acid.

PT SIGNAL; 1 18  
 PT CHAIN; 19 436  
 PT CHAIN; 19 378  
 PT PEPTIDE; 380 388  
 PT CHAIN; 389 436  
 PT DOMAIN; 19 135  
 PT DOMAIN; 136 257  
 PT DOMAIN; 258 378  
 PT MOD\_RBS; 19 19  
 PT CARBOHYD; 87 67  
 PT CARBOHYD; 136 136  
 PT CARBOHYD; 168 168

PT CARBOHYD; 197 197  
 PT CARBOHYD; 204 204  
 PT DISULPID; 27 406  
 PT DISULPID; 82 93  
 PT DISULPID; 106 125  
 PT DISULPID; 141 144  
 PT DISULPID; 205 217  
 PT DISULPID; 228 247  
 PT DISULPID; 263 266  
 PT DISULPID; 327 339  
 PT DISULPID; 350 369  
 PT CONFLICT; 295 295  
 SQ SEQUENCE 436 AA: GLYXSIYPIARETTCSKGSNELTELTKSCEBVKYPTV 64  
 SQ SEQUENCE 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;  
 Query Match Score 440; DB 1; Length 436,  
 Best local Similarity 70.4%; Proc. No. 1; Be 34;  
 Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 4 KDPVQPPTRKICPGCPDIPNTSPELLETLTITLNAAENNTYKIDIVKVKARVOVA 63  
 Db 253 KDPVQPPTRALCGCPKIPDVDSDEPLPSIAGLNBDGAYPKIDVVKATQVVA 312

QY 64 GRKYPIDPVAETTSKEENEELTTSCTERKQGDNCATVYVPPWEKCIPTV 118  
 Db 313 GLYSIYPIARETTCSKGSNELTELTKSCEBVKYPTV 367

RESULT<sup>3</sup>  
 KRH\_BOVIN STANDARD; PRT; 621 AA.  
 ID KRH\_BOVIN  
 AC P01044;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-PB-2003 (Rel. 41, Last annotation update)  
 DE Kininogen, HKW I precursor (thiol protease inhibitor) [Contains:  
 DE Bradykinin] [Bovine].  
 OS Bos taurus [Bovine].  
 OC Sukanya; Metacosa; Chordata; Vertebrata; Euteleostomi;  
 OC Kitamura N.; Takagaki Y.; Furuto S.; Tanaka T.; Nawa H.; Nakanishi S.;  
 OC Miyata T.; Iwanga S.;  
 OC Bovidae; Bovinae; Bos.  
 OC BOVINE TAXID=9913;  
 RN 1  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=4404106; PubMed=6571699;  
 RX MEDLINE=87137530; PubMed=35462951;  
 RA Kitamura N.; Takagaki Y.; Furuto S.; Tanaka T.; Nawa H.; Nakanishi S.;  
 RA Miyata T.; Iwanga S.;  
 RA "A single gene for bovine high molecular weight and low molecular weight kininogens."  
 RT weight kininogen.  
 RL NATURE 305:545-549 (1983).  
 RN 12  
 RP SEQUENCE OF 19-378.  
 RX MEDLINE=87137530; PubMed=35462951;  
 RX MEDLINE=87137530; PubMed=35462951;  
 RA Sueyoshi T.; Miyata T.; Hayashida H., Kato H., Hayashida H.,  
 RA "Bovine high molecular weight kininogen. The amino acid sequence, RT positions of carbohydrate chains and disulfide bridges in the heavy chain portion."  
 RA Kato H., Nagasawa S., Suzuki T.; Suzuki T.;  
 RA studies on the structure of bovine kininogen-I, II, RT bonds and of methionyl bonds in kininogen-II.  
 RN 13  
 RP SEQUENCE OF 378-393.  
 RX MEDLINE=70180420; PubMed=4986212;  
 RX MEDLINE=70180420; PubMed=4986212;  
 RA Kato H., Nagasawa S., Suzuki T.;  
 RA "Studies on the structure of bovine kininogen-I, II, RT bonds and of methionyl bonds in kininogen-II."  
 RN 14  
 RP SEQUENCE OF 458-498.  
 RX MEDLINE=75170265; PubMed=116937;  
 RX MEDLINE=75170265; PubMed=116937;  
 RA Han Y.N.; Keniya M.; Iwanaga S.; Suzuki T.;  
 RA "Studies on the primary structure of bovine high-molecular-weight  
 RT kininogen. Amino acid sequence of a fragment (histidine-rich  
 RT peptide), released by Plasma kallikrein."  
 RT J. Biochem. 77:55-68 (1975).  
 RL J. Biochem. 77:55-68 (1975).  
 CC - FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)

CC HMW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins); (4F) it has a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action).

## 4.1. ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;  
 CC IsoID="P01046-1"; Sequence=Displayed;  
 CC Name=HMW\_I;  
 CC IsoID="P01046-1"; Sequence=External;  
 CC TISSUE\_SPECIFICITY: Plasma.  
 CC PTM: Bradykinin is released from kininogen by plasma kallikrein.

CC SIMILARITY: Contains 3 cystatin-like domains.

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CC DR EMBL: V01491; CA22735.1; ~.

CC DR InterPro: IPI0002195; Cystatin.

CC DR InterPro: IPI000010; Kininogen.

CC DR PRINTS: PRO034; CYTATIN; 3.

CC DR SMART: SM00043; CYTATIN; 3.

CC DR PROSITE: PS000287; CYTATIN; 2. Glycoprotein, Plasma, Repeat, Vasoconstrictor, Thrombolytic inhibitor; Bradykinin, Blood coagulation, Inflammatory response; Signal, Pyrolydine carboxylic acid.

CC FT CHAIN 1 18 SIGNAL  
FT CHAIN 19 621 KININONE, HMW\_I.  
FT CHAIN 19 378 HEAVY CHAIN.  
FT CHAIN 19 388 LIGHT CHAIN.  
FT PEPTIDE 380 621 BRADYKININ.

CC PT DOMAIN 19 135 CYSTATIN-LIKE 1.  
PT DOMAIN 136 257 CYSTATIN-LIKE 2.  
PT DOMAIN 258 378 CYSTATIN-LIKE 3.  
PT MOD\_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.  
PT CARBOHYD 87 87 N-LINKED (GLCNAC, .).  
PT CARBOHYD 136 136 O-LINKED (PARTIAL).  
PT CARBOHYD 168 168 N-LINKED (GLCNAC, .) (OR 169).  
PT CARBOHYD 197 197 N-LINKED (GLCNAC, .) (PARTIAL).  
PT CARBOHYD 204 204 N-LINKED (GLCNAC, .).  
PT DISULFID 27 591 INTERCHAIN.  
PT DISULFID 82 91  
PT DISULFID 106 125  
PT DISULFID 141 144  
PT DISULFID 205 217  
PT DISULFID 228 247  
PT DISULFID 263 266  
PT DISULFID 327 339  
PT DISULFID 350 369  
SQ SEQUENCE 621 AA; 68890 MW; D16850BEFE3C55CD CRC64;

CC	Db	253	KDFVQPPTKICVGCPDRIDPTNSPELEETUTITKNAENNATPFKIDNVKKARYQQVA
CC	Qy	64	GKRYVDFVARETTCSKSNEELTSCTKLGSLOCNAEVVWEEKKVPYTV
CC	Db	313	GLKYSIVPIARETTCSKSNEELTSCEINHGQILHCDANTYVWEEKVYPTV
CC	Db	210	DBP01046-1
CC	Db	21-JUL-1986	(Rel. 01, Created)
CC	Db	15-MAR-2004	(Rel. 43, Last annotation update)
CC	DB	Kininogen, HMW II precursor (thio protease inhibitor) (Contains: ID_KIN2_BOVIN STANDARD, PRT: 434 AA.	
CC	AC	P01046-1	
CC	DT	21-JUL-1986	
CC	DT	15-MAR-2004	
CC	DB	Kininogen, HMW II precursor (thio protease inhibitor) (Contains: ID_KIN2_BOVIN STANDARD, PRT: 434 AA.	
CC	DS	Bradykinin	
CC	OS	Bos taurus (Bovine)	
CC	OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.	
CC	OX	NCBI_TaxID:9913;	
CC	RN	[1]	
CC	RP	SEQUENCE FROM N.A.	
CC	RP	Medline=3111859; PubMed=6572010;	
CC	RA	Nava H., Kitamura N., Hirose T., Asai M., Inayama S., Nakaneishi S.,	
CC	RT	Primary structures of bovine liver low molecular weight kininogen precursors and their two mRNAs.	
CC	RT	Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).	
CC	RL	[2]	
CC	RN	SEQUENCE OF 19-376.	
CC	RP	Medline=71131530; PubMed=3546295;	
CC	RA	Suematsu T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.,	
CC	RA	Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).	
CC	RP	Sequence of 19-376.	
CC	RA	Medline=71131530; PubMed=3546295;	
CC	RA	Suematsu T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.,	
CC	RA	Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).	
CC	CC	"Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion."	
CC	RL	J. Biol. Chem. 262:2768-2779 (1987).	
CC	CC	"Kininogens are inhibitors of the aggregation of thrombocytes; (2) the active peptide kallidin that is released from LMW-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction, (3B) induction of hypertension, (3C) natriuresis and diuresis (kidney)."	
CC	CC	- SUBCELLULAR LOCATION: Extracellular.	
CC	CC	- ALTERNATIVE PRODUCTS:	
CC	CC	Event=Alternative splicing; Named isoforms=2;	
CC	CC	Name=HMW_II;	
CC	CC	IsoId=P01047-1; Sequence=Displayed;	
CC	CC	Name=HMW_II;	
CC	CC	IsoId=P01045-1; Sequence=External;	
CC	CC	- TISSUE SPECIFICITY: Plasma.	
CC	CC	- PTM: Bradykinin is released from kininogen by plasma kallikrein.	
CC	CC	- MISCELLANEOUS: LMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting.	
CC	CC	- SIMILARITY: Contains 3 cystatin-like domains.	
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
DR	DR	V00427; CAA23710.1; -	
DR	DR	PTR; A01284; KG0102.	
DR	DR	HS38; P01038; IA90.	
DR	DR	InterPro; IPR000010; Cystatin.	
DR	DR	Pfam; PF00031; Cystatin_3.	
DR	DR	SMART; SM00043; Cystatin_3.	
DR	DR	PROSITE; PS00287; Cystatin_2.	
DR	DR	Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;	

Query Match 64.0%  
 Best Local Similarity 70.4%  
 Matches 81; Conservative 14; Missmatches 20; Indels 0; Gaps 0;

4 KDFVQPPTKICVGCPDRIDPTNSPELEETUTITKNAENNATPFKIDNVKKARYQQVA 63

KW Thiol protease inhibitor; Bradykinin; Signal;  
 KW Pyrrolidone carboxylic acid.  
 PT SIGNAL 1  
 PT CHAIN 19 434 KININOGEN, HMW II.  
 PT CHAIN 19 376 HEAVY CHAIN.  
 PT PEPTIDES 378 384 BRADYKININ.  
 PT CHAIN 387 434 LIGHT CHAIN.  
 PT DOMAIN 19 135 CYSTATIN-LIKE 1.  
 PT DOMAIN 136 256 CYSTATIN-LIKE 2.  
 PT DOMAIN 257 376 CYSTATIN-LIKE 3.  
 PT MOD RES 19 139 PYRROLIDONE CARBOXYLIC ACID.  
 PT CARBOHYD 87 67 N-LINKED (GLCNAC).  
 PT CARBOHYD 136 136 O-LINKED (PARTIAL).  
 PT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (OR 169).  
 PT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).  
 PT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).  
 PT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).  
 PT DISULFID 27 404 INTERCHAIN.  
 PT DISULFID 82 93  
 PT DISULFID 106 125  
 PT DISULFID 141 144  
 PT DISULFID 205 217  
 PT DISULFID 228 247  
 PT DISULFID 261 264  
 PT DISULFID 325 337  
 PT DISULFID 348 367  
 SQ SEQUENCE 434 AA; 48148 MW; 73A7079DE1E03430 CRC64;  
 Query Match Similarity 60.1%; Score 413.; DB 1; Length 434;  
 Best Local Similarity 67.2%; Pred. No. 6; 6e-32;  
 Matches 78; Conservative 14; Mismatches 22; Indels 2; Gaps 1;  
 Qy 3 GDFDVQOPTKIGVGRDPIPTNSPELTSTLTTITLNAAENNAPYKIDVNYKARYQQV 62  
 Db 252 GDBPL--PDMVQGKPKPVDSDLEALNSVIAKNAEDGPPFKIDVYKARYQV 309  
 Qy 63 AGKKYPPDVIARETCSKESNEZLTSCTKQLGOLDMAENTVPMEEKVKYPTV 118  
 Db 310 GLKLYSPVPIARETCSKGANEELTKSCSININGQTHCDANVVPMEKVKYPTV 365

RESULT 5

KNH2\_BOVIN STANDARD PRT; 619 AA.

AC PO015;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 01, Last annotation update)

DE Kininogen HMW II precursor (thiol protease inhibitor) (Contains:  
 DE Bradykinin]  
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Ruminantia; Pecora; Bovidae;  
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae;  
 OC Bovidae; Bovinae; Bovidae;  
 OC NCBI\_TAXID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:84014106; PubMed:6571699;

RX Kicemura N., Takigaki Y., Furuto S., Tanaka T., Nawa H., Nakashishi S., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S., Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.,

RT "Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion.", J. Biol. Chem. 262:2768-2779(1987).

RN [3]

RP SEQUENCE OF 376-391.

PT DOMAIN	257	376	CYSTATIN-LIKE 3.		Pereira G., Pesole G.,
PT MOD RES	19	19	PYRROLIDONE CARBOXYLIC ACID.		
PT CARBOHYD	87	87	N-LINKED (GLCNAc).		RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
PT CARBOHYD	136	136	O-LINKED (PARTIAL).		RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
PT CARBOHYD	168	168	N-LINKED (GLCNAc. . .) (OR 169).		RA Sandelin A., Schneider C.A., Sehou M., Shimada K.,
PT CARBOHYD	197	197	N-LINKED (GLCNAc. . .) (PARTIAL).		RA Sultana R., Takehara Y., Taylor M.S., Teasdale R.D., Tomita M.,
PT CARBOHYD	204	204	N-LINKED (GLCNAc. . .).		RA Verardo R., Wagner L., Whalestedt C., Wang Y., Watanabe Y., Wells C.,
PT CARBOHYD	280	280	N-LINKED (GLCNAc. . .).		RA Wilming L.G., Wyrshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
PT CARBOHYD	400	400	O-LINKED.		RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Carninci P., Hayatsu N.,
PT DISULFID	27	589	Kondo S., Sakatani H., Kohno H., Nakamura K., Arakawa T., Fukuda S.,		RA Hirozane-Kishikawa T., Waki K., Kawai J., Aizawa K.,
PT DISULFID	92	93	Habizume W., Imotani K., Ishii Y., Itoh M., Kagaya I.,		RA Shiraki T., Waki K., Kawai J., Aizawa K.,
PT DISULFID	106	125	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shigenawa A.,		RA Miyazaki A., Sakai K.,
PT DISULFID	141	144	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,		RA Birney E., Hayashizaki Y.,
PT DISULFID	205	211	"Analysis of the mouse transcriptome based on functional annotation of		RT RT
PT DISULFID	228	247	PT DISULFID		RT 60,770 full-length cDNAs.",
PT DISULFID	261	264	PT DISULFID		RL Nature 420:563-573 (2002).
PT DISULFID	325	337	PT DISULFID		RN [13]
PT DISULFID	348	367	PT VARIANT		RC SEQUENCE FROM N.A. (ISOFORM LMW).
PT VARIANT	401	404	PT VARIANT		RX MEDLINE=22182571; PubMed=12477932;
SO SEQUENCE	619 AA,	6710 MW,	SEQUENCE		RA Kraatzburg R.L., Peingold B.A., Grouse L.H., Darge J.G., Schuler G.D.,
					RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
					RA Altschul S.P., Buetow K.H., Schaefer C.F., Bhat N.K.,
					RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh P.,
					RA Ditschenko L., Marulina K., Farmer A.A., Rubin G.M., Hong L.,
					RA Stapleton M., Scores M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
					RA Brownstein M.J., Uedin T.B., Toshimori S., Carninci P., Prange C.,
					RA Rosa S.S., Loquicano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,
					RA Rosek S.A., McEwan P.J., McKernan K.J.A., Malek J.A., Gunnarson P.H.,
					RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
					RA Villalobos D.K., Huzny D.M., Bodenreger B.J., Lu X., Gibbs R.A.,
					RA Pahay J., Heiton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
					RA Whiting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
					RA Blakesley R.W., Touchman J.W., Green S.D., Dickson M.C.,
					RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
					RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
					RA Scherzer A., Schein J.E., Jones J.M., Marrs M.A.,
					RT "Generation and initial analysis of more than 15,000 full-length
					RL proc. Natl. Acad. Sci. U.S.A. 99:16839-16903 (2002).
					CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
					CC HMW-kininogen plays an important role in blood coagulation by helping to position optimally prokallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects; (4A) influence in smooth muscle contraction; (4B) induction of hypotension; (4C) natriuresis and diuresis; (4D) decrease in blood glucose level; (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability; (4B2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins); (4F) it has a cardioprotective effect (directly via endothelium-derived relaxing factor action); (5) HMW-kininogen inhibits the aggregation of thrombocytes; (6) HMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting (By similarity).
					CC -1- SUBCELLULAR LOCATION: Secreted.
					CC -1- ALTERNATIVE PRODUCTS:
					CC Event=Alternative splicing; Named isoforms=2;
					CC Name=HMW; Sequence=displayed;
					CC IsoId=008677-1; Sequence=VSP_001264;
					CC Name=LMW;
					CC IsoId=008677-2; Sequence=VSP_001263; VSP_001264;
					CC -1- TISSUE SPECIFICITY: Plasma.
					CC -1- PTM: Bradykinin is released from kininogen by plasma kallikrein.
					CC -1- SIMILARITY: Contains 3 cystatin-like domains.
					CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation, the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.ibb-bib.ch/announce/> or send an email to license@ibb-bib.ch).

CC	NCBI_TaxID:10116;
CC	OX RN [1]
CC	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
CC	RP
CC	RX MEDLINE:87137443; PubMed=3039065;
CC	RX MEDLINE:86100826; PubMed=2413018;
CC	RX MEDLINE:86100826; PubMed=2413018;
CC	RA Kikugawa H., Kitamura N., Hayashida H., Miyata T., Nakaniishi S., "Differing expression patterns and evolution of the rat kininogen genes family," RT J. Biol. Chem. 262:12981298(1987).
CC	RN [2]
CC	SEQUENCE FROM N.A. (ISOFORM LMW).
CC	RP
CC	RX MEDLINE:86100826; PubMed=2413018;
CC	RA Furuto-Kato S., Matsumoto A., Kitamura N., Nakaniishi S., "Primary structures of the mRNAs encoding the rat preproenzymes for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor," RT J. Biol. Chem. 260:12054-12059(1985).
CC	RT
CC	RT
CC	RL J. Biol. Chem. 260:12054-12059(1985).
CC	RN [3]
CC	SEQUENCE OF 1-65 FROM N.A.
CC	RP
CC	RC STRAIN=BUFFALO;
CC	RX MEDLINE:8720580; PubMed=2419509;
CC	RA Pung W.-P., Schreiber G., "Structure and expression of the genes for major acute phase alpha 1-protein (thiostatin) and kininogen in the rat," RT J. Biol. Chem. 262:9298-9308(1987).
CC	RL J. Biol. Chem. 262:9298-9308(1987).
CC	RN [4]
CC	SEQUENCE OF 1-41 FROM N.A.
CC	RP
CC	RC STRAIN=ISTER; TISSUE=LIVER;
CC	RX MEDLINE:8711765; PubMed=3810598;
CC	RA Kagiyama R., Kitamura N., Ohkubo H., Nakaniishi S., "Differing utilization of homologous transcription initiation sites of rat K and T-kininogen genes under inflammation condition," RT J. Biol. Chem. 262:2345-2351(1987).
CC	RL J. Biol. Chem. 262:2345-2351(1987).
CC	-I- FUNCTION: (1) Kininogens are inhibitors of trypsinases, (2) HMW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the thrombin-and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E2), release of other mediators of inflammation (e.g. Prostaglandins), (4F) it has a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action); (5) HMW-kininogen inhibits the aggregation of thrombocytes; (6) HMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting.
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- ALTERNATIVE PRODUCTS: Secreted.
CC	Event=Alternative splicing; Named isoforms=2;
CC	IsoId=P08934-1; Sequence=Displayed,
CC	Name=HMW_KININOGEN; Name=LMW_KININOGEN;
CC	IsoId=P08934-2; Sequence=VP_001266;
CC	-I- TISSUE SPECIFICITY: Plasma.
CC	-I- PTM: Bradykinin is released from kininogen by Plasma kallikrein.
CC	-I- MISCELLANEOUS: Rat expresses four types of kininogens: the classical HMW/LMW kininogens and two additional low-like kininogens: T-I and T-II.
CC	-I- SIMILARITY: Contains 3 cystatin-like domains.
CC	This WIGS-PROT entry is copyright. It is produced through collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ibb-bib.ch/announce/">http://www.ibb-bib.ch/announce/</a> or send an email to license@ibb-bib.ch).
CC	EMBL; L28429; AB414866.1; -.



Best Local Similarity 62.1% Prod. No. 1.6e-29;保守性 15; Mismatches 29; Indels 0; Gaps 0;  
Matches 72;

Qy 3 GGDPPDPTKICVGPPDIPPTNSPBLSTLTITLNAENNATTPYKIDVVKARVQV 62  
Db 252 GDDLFULLPKXCKFCGCPKPNIPVDPSPBLKALGHISIAQLNAGHNLHYPKIDVVKARVQV 311

Qy 63 ACKKYPIDFVARBTCSKESNELTSETKKGSDMAYEVTVPEKLYPTV 118  
Db 312 ACTKVTEPIARTCSKOTNTLTADECTKHGQSLNCHNMRPHENKVPTV 367

**RESULT 9**  
KRTH\_RAT ID ROTTI\_RAT STANDARD; PRT; 430 AA.

AC P010781\_P004081; ID R01\_03; Created) DT 01-NOV-1986 (Rel. 09, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DB T-kininogen I Precursor (Major acute phase protein) (Alpha-1-MAP)  
DE (Thiosatin; T-kinin).  
GN MAPL.

OS Rattus norvegicus (Rat).

RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI\_TaxId=10116; [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-8608265; PubMed=2413018;

RA Purito-Kato, S.; Matsumoto A.; Kitamura N.; Nakaniishi S.,

RT "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine protease inhibitor".

RT J. Biol. Chem. 260:12054-12059(1985).

RN [2]

RP SEQUENCE OF 5'-430 FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE-8608265; PubMed=2413019;

RA Anderson K.P., Heath P.C.,

RT "The relationship between rat major acute phase protein and the kininogens", J. Biol. Chem. 260:12065-12071(1985).

RN [3]

RP SEQUENCE OF 7-430 FROM N.A.

RX MEDLINE-85121561; PubMed=257892;

RA Cole T., Inglis A.S.; Roxburgh C.M.; Howlett G.J.; Schreiber G.,

RT "Major acute phase alpha 1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.",

RT FEBS Lett. 182:57-61(1985).

RN [4]

RP SEQUENCE OF 1-565 FROM N.A.

RX MEDLINE=17250580; PubMed=439809;

RA Fung W.-P.; Schreiber G.,

RT "Structure and expression of the genes for major acute phase alpha 1-protein (thiosatin) and kininogen in the rat.",

RT J. Biol. Chem. 262:928-9308(1987).

CC -I- FUNCTION: Kininogens are plasma glycoproteins with a number of functions: (1) as precursor of the active peptide bradykinin they effect smooth muscle contraction, induction of hypotension and increase of vascular permeability. (2) They play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. (3) They are inhibitor of thrombolytic processes.

CC -I- SUBCELLULAR LOCATION: Extracellular.

CC -I- TISSUE SPECIFICITY: Plasma.

CC -I- INDUCTION: In response to an inflammatory stimulant. T-kininogen

CC II synthesis is induced and the plasma concentration of T-kininogen I is raised.

CC -I- PTM: As T-kininogen I is raised, it is not released from its precursor by either tissue or plasma kallikrein.

CC -I- MISCELLANEOUS: Rate express four types of kininogens: the

classical LwW and LwW kininogens produced by alternative splicing of the same gene, and two additional LwW-like kininogens: T-I and T-II.  
CC -I- SIMILARITY: Contains 3 cystatin-like domains.  
CC -I- CAUTION: In addition to the conflicts described in the feature CC table, Ref.2 sequence differs from that shown in Positions 257, CC 262, 269, 295, 314, 311, 332 and 359. In all those positions the alternate amino acid is the one present in T-II CC kininogen.  
CC -I- This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation CC in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by commercial CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).  
CC -I- DR EMBL; M11881; AAA41489-1; -  
CC -I- DR EMBL; M11667; AAA41510-1; -  
CC -I- DR EMBL; M16454; AAA41168-1; -  
CC -I- DR SMART; SM00032; CY\_3; -  
CC -I- DR PROSITE; PS00287; CYSTATIN\_2.  
CC -I- DR Glycoprotein Plasma, Repeat, Vasodilator, Multigene family, Acute phase, Signal.  
CC -I- KW Thiol Protease Inhibitor; Bradykinin; Acute phase; Signal.  
CC -I- PT SIGNAL 18  
CC -I- PT CHAIN 19  
CC -I- PT CHAIN 19  
CC -I- PT PEPTIDE 376  
CC -I- PT CHAIN 387  
CC -I- PT DOMAIN 19  
CC -I- PT DOMAIN 136  
CC -I- PT DOMAIN 258  
CC -I- PT DISULFID 28  
CC -I- PT DISULFID 83  
CC -I- PT DISULFID 107  
CC -I- PT DISULFID 141  
CC -I- PT DISULFID 205  
CC -I- PT DISULFID 228  
CC -I- PT DISULFID 263  
CC -I- PT DISULFID 327  
CC -I- PT DISULFID 350  
CC -I- PT CARBOHYD 82  
CC -I- PT CARBOHYD 126  
CC -I- PT CARBOHYD 168  
CC -I- PT CARBOHYD 204  
CC -I- PT CARBOHYD 326  
CC -I- PT CARBOHYD 328  
CC -I- PT CONFLICT 26  
CC -I- PT CONFLICT 55  
CC -I- PT CONFLICT 61  
CC -I- PT CONFLICT 83  
CC -I- PT CONFLICT 166  
CC -I- PT CONFLICT 179  
CC -I- PT CONFLICT 193  
CC -I- PT CONFLICT 212  
CC -I- PT CONFLICT 214  
CC -I- PT CONFLICT 229  
CC -I- PT CONFLICT 233  
CC -I- PT CONFLICT 257  
CC -I- PT CONFLICT 262  
CC -I- PT CONFLICT 264  
CC -I- PT CONFLICT 268  
CC -I- PT CONFLICT 295  
CC -I- PT CONFLICT 314  
CC -I- PT CONFLICT 332  
CC -I- PT CONFLICT 389  
CC -I- DR > O (IN REF. 2).  
CC -I- DR > K (IN REF. 2).  
CC -I- DR > F (IN REF. 2).  
CC -I- DR > Y (IN REF. 2).  
CC -I- DR > H (IN REF. 2).  
CC -I- DR > R (IN REF. 2).  
CC -I- DR > Y (IN REF. 2).  
CC -I- DR > S (IN REF. 2).  
CC -I- DR > D (IN REF. 2).  
CC -I- DR > P (IN REF. 2).  
CC -I- DR > H (IN REF. 2).  
CC -I- DR > R (IN REF. 2).  
CC -I- DR > Y (IN REF. 2).  
CC -I- DR > S (IN REF. 2).  
CC -I- DR > N (IN REF. 2).  
CC -I- DR > L (IN REF. 2).  
CC -I- DR > K (IN REF. 2).  
CC -I- DR > Q (IN REF. 2).

PT CONFLICT 414 414 R->G (IN REP. 2 AND 3).  
 PT CONFLICT 415 415 A->L (IN REP. 2).  
 PT CONFLICT 420 421 D->E (IN REP. 3).  
 PT CONFLICT 430 430 P->S (IN REP. 1).  
 SEQUENCE 430 AA; MW: PAEBB78PAF423C3 CRC64;  
 Query Match 55.3% Score 360, DB 1, Length 430;  
 Best Local Similarity 62.1%, Pred. No. 9e-29;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;  
 Qy 3 GKDPPQPRKICGCCPAPDIPNSRERETHTITKAENRTATPKIDNQKARVQV 62  
 Db 252 GDDLFELLPRNGCPREIPDSPEKLEAQLAQRHHPYKIDTVKCATSQV 311  
 Qy 63 AGKRYPIDFVARETTCSKESNEELTESCENPKLQ-QSISDNCAVYVPPWEEKIYPV 118  
 Db 312 AGVIVVIBIARTNCQSKELTADCEPKHQLQSINCNANVYSPWENKVVTV 367

RESULT 10  
 CYTP\_MOUSE ID CYTP MOUSE STANDARD PRT/ 144 AA.  
 AC 0890581/  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 42, Last annotation update)  
 DB Cystatin P Precursor (Leukocystatin) (Cystatin 7) (Cystatin-like protein) (CMAP).  
 DB metastasis-associated protein (CMAP).  
 GN CN  
 OS Mus musculus (Mouse).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9906/  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-#829157; PubMed=9632704/  
 RA Halton S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,  
 RA Weiss M., Ikeda M., Liggett D., Heimb A., Caux C., Lebecque S.,  
 RA Hamm C., Menon S., McClanahan T., Gorman D., Zurawski G.,  
 RT "Leukocystatin, a new class II cystatin expressed selectively by  
 RA hematopoietic cells".  
 RL J. Biol. Chem. 273:16400-16408 (1998).  
 CC -: FUNCTION: Inhibits papain and cathepsin L but with affinities  
 CC lower than other cystatins. May play a role in immune regulation.  
 CC through inhibition of a unique target in the hematopoietic system.  
 CC - SUBCELLULAR LOCATION: Secreted (Probable).  
 CC - SIMILARITY: Belong to the Cystatin Family.

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 or send an email to license@ebi-sib.ch).

CC DR EMBL; AP031026; AAC0140.1; -.  
 DR HSSP; P01039; ICG96.  
 DR MGDB; MGI:1198217; Cst7.  
 DR InterPro; IPI0000010; Cystatin.  
 DR Pfam; PF00001; cystatin.  
 DR SMART; SM00043; CY\_1.  
 PT PROSITE; PS00287; CYSTATIN; FALSE NEG.  
 KW Thiol protease inhibitor; Glycoprotein; Signal.  
 PT SIGNAL 1 18 POTENTIAL.  
 PT CHAIN 1 18 CYSTATIN.  
 PT ACT SITE 36 144 REACTIVE SITE.  
 PT SITE 80 84 SECONDARY AREA OF CONTACT.  
 PT DISULFID 98 109 BY SIMILARITY.  
 PT DISULFID 123 143 BY SIMILARITY.  
 SEQUENCE 144 AA; 16380 MW; B5837334C1B4A89C CRC64;

Query Match 25.0% Score 171.5, DB 1, Length 144;  
 Best Local Similarity 35.5%, Pred. No. 1.7e-09;  
 Matches 39; Conservative 22; Mismatches 42; Indels 7; Gaps 3;  
 Qy 4 KDPVOPPTKICVCPDPIPTSPETLTITKLAKENNTATPYKIDNQKARVQVVA 63  
 Db 27 KDLI---SSVKPVPKTTANPGTLKAARSHVEKFNCNTDIPLESVSKALVQYK 83  
 Qy 64 GKRYPIDFVARETTCSKESNEELTSCE--TKLKGQSLDCAEVTPW 110  
 Db 84 GLKYMLEVIGRITTCRKTMMHQL-DNCIDPQTNPALKRTFLCYSEWVTPW 132

RESULT 11  
 CYTP\_HUMAN ID CYTP HUMAN STANDARD PRT/ 145 AA.  
 AC 076056; OSUED4/  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-Oct-2003 (Rel. 42, Last annotation update)  
 D2 Cystatin P precursor (Leukocystatin) (Cystatin 7) (Cystatin-like protein) (CMAP).  
 DB metastasis-associated protein (CMAP).  
 GN CST7.  
 OS Homo sapiens (Human).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9906/  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-#98400133; PubMed=9733783/  
 RA Ni J., Fernandez M.A., Danielsson L., Chilakuru R.A., Zhang J., Grubb A., Su J., Gentz R., Abramson M.,  
 RA Xu Y., Weiss M., Ikeda M., Liggett D., Heimb A., Caux C., Lebecque S., Hamm C., Menon S., McClanahan T., Gorman D., Zurawski G.,  
 RT "Cystatin P is a Glycosylated human low molecular weight cysteine proteinase inhibitor.".  
 RL J. Biol. Chem. 273:24797-24804 (1998).  
 RN 121  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-#98298157; PubMed=9632704/  
 RA Halton S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,  
 RA Weiss M., Ikeda M., Liggett D., Heimb A., Caux C., Lebecque S.,  
 RA Xu Y., Weiss M., Ikeda M., Liggett D., Heimb A., Caux C., Lebecque S., Hamm C., Menon S., McClanahan T., Gorman D., Zurawski G.,  
 RT "Leukocystatin, a new class II cystatin expressed selectively by hematopoietic cells."  
 RL J. Biol. Chem. 273:16400-16408 (1998).  
 RN 131  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-#2039571; PubMed=10945474/  
 RA Morita M., Arakawa H., Yoshiuchi N.;  
 RT "Human homologue of murine CMAP".  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN 141  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-#21638719; PubMed=11780052/  
 RA Delcukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggsley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beare D.M., Brown A.J.,  
 RA Beasley O.P., Bird C.P., Blahey S.E., Bridgeman A.M., Carter N.P.,  
 RA Buck D., Burill W.D., Butler A.P., Carter J.C., Clark G., Clark L.N., Clark S.Y., Clees C.M.,  
 RA Chapman J.C., Clamp M., Collier R.S., Connor R.B., Corby N.R.,  
 RA Conlon A., Coville J., Deadman R., Dhami D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., He S., Holden J.L., Holden P.J.,  
 RA Huckle P., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lehvastalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H., Rice C.M., Ross M.T., Scott C.B., Gehra H.K., Showken R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Stelton J.E., Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tramans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J., "The DNA sequence and comparative analysis of human chromosome 20.", RL Nature 414 865-871(2001).  
 (6)

SEQUENCE FROM N.A.

TISSUE:Lung; PMID=2288257; PubMed=12477932;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuster G.D., Altschul S.P., Zeeberg B., Buetow K.H., Schuster G.D., Blatner R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.P., Marinica K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marzina K., Casavant T.L., Scheetz T.E., Stotleton M., Soates M.B., Sonnino M.P., Casavant T.L., Prange C., Brownstein M.J., Usain T.B., Tohbyuki S., Carninci P., Prangle C., Rahm S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaillon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman J.A., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimes J.S., Schmidt J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalicka U., Smalius D.E., Scherzer A., Schein J.E., Jones S.J.M., Marrs M.A./ RT PROTEIN: Inhibit Papain and cathepsin L but with affinities lower than other cystatins. May play a role in immune regulation human and mouse cDNA sequences." RT PROTEIN: Inhibit Papain and cathepsin L but with affinities lower than other cystatins. May play a role in the hematopoietic system.  
 -I- SUBCELLULAR LOCATION: Secreted (Probable).  
 -I- TISSUE SPECIFICITY: Primarily expressed in peripheral blood cells and spleen.  
 -I- SIMILARITY: Belongs to the cystatin family.

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DR EMBL; AP036342; AAC35347.1/-.  
 DR BMBL; AP0184; AAC39788.1/-.  
 DR BMBL; AB015235; BAA34341.1; ALT\_INIT.  
 DR EMBL; AB029616; BAB1086.1; ALT\_INIT.  
 DR EMBL; AB035651; CAB75598.1; "-.  
 DR EMBL; BC015507; ARH15507.1; ALT\_INIT.  
 DR HSSP; P01034; 1G96.  
 DR Genev; HGNC:2479; CST7.  
 DR MM: 603253; "-.  
 DR GO; GO:004869; P:cysteine protease inhibitor activity; TAS.  
 DR GO; GO:006695; P:immune response; TAS.  
 DR InterPro; IPR00010; Cystatin.  
 DR Pfam; PP00031; cystatin\_1.  
 DR PROSITE; PS00087; CYSTATIN; CY1.  
 DR PROSITE; PS00087; CYSTATIN; CY1.  
 DR ThioI protease inhibitor; Glycoprotein; signal.

KW SIGNAL 1 19 POTENTIAL,  
 PT CHAIN 20 145 CYSTATIN P.  
 PT ACT\_SITE 37 REACTIVE SITE.

Query Match 20.2%; Score 118 5; DB 1; Length 146!  
 Best Local Similarity 27.9%; Pred. No. 2.4e-06; Indels 11; Gaps 4;  
 Matches 34; Conservative 25; Mismatches 52;

**RESULT 13**

CYTOM HUMAN STANDARD; PRT; 149 AA.

ID CYTM\_HUMAN  
AC Q15818;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)

DB Cystatin M precursor (Cystatin E).

GN C876.

OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;

RN [1] \_

RP SEQUENCE FROM N.A.

RX MEDLINE-#7150844; PubMed:89953180]

RA Sotiropoulou G., Andowicz A., Sager R.,  
RT "Identification, cloning, and characterization of cystatin M, a novel  
RT cysteine proteinase inhibitor, down-regulated in breast cancer.",  
RN [2] J. Biol. Chem. 272:903-910(1997).

RP SEQUENCE FROM N.A.

RA Ni J., Abramson M., Zhang M., Fernandez M.A., Grubb A., Su J.,  
RA Yu G.L., Li Y., Parmelee D., King L., Coleman T.A., Gentz S.,  
RA Thorakura R., Nguyen N., Hesselberg M., Gentz R.,  
RT "Cystatin E is a novel human cysteine proteinase inhibitor with  
RT structural resemblance to family 2 cystatins.",  
RL J. Biol. Chem. 272:10953-10958(1997).  
RN

RC TISSUE="prostate",  
RX MEDLINE-#23318257; PubMed:12479327;

RA Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G., Schulter G.D.,  
RA Klausner R.D., Collinge F.S., Wagner L., Shemesh C.M., Schaefer C.P., Bhat N.K.,  
RA Altschuler S.P., Zeeberg B., Buetow K.H., Schaffer C.P., Blat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heilek F.,  
RA Diatchenko L., Marusina K., Palmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Tsohlyuki S., Cornblit P., Prange C.,  
RA Raju S.S., Loqueland J.N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalain D.K., Muzdy D.M., Sodergren P.J., Ju X., Gibbs R.A.,  
RA Pahey J., Heilton S., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickeson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schatz A., Schein J.B., Jones S.J.M., Marras M.A.;  
RT Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences",  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [4] CHARACTERIZATION, AND TISSUE SPECIFICITY.

RX MEDLINE=21246810; PubMed:11348477;

RA Zeulman P.L., Van Vlijmen-Willems I.M., Jansen B.J., Sotiropoulou G.,  
RA Curfs J.H., Meij J.P., Janssen J.J., Van Ruissen P., Schalkwijk J.,  
RT "Cystatin M/E expression is restricted to differentiated epidermal  
keratinocytes and sweat glands: a new skin-specific proteinase",

RT Inhibitor that is a target for cross-linking by transglutaminase";  
RL J. Invest. Dermatol. 115:693-701(2001).  
CC "- FUNCTION: Shows moderate inhibition of cathepsin B but is not  
CC active against cathepsin C.  
CC - SUBCELLULAR LOCATION: Secreted to the stratum granulosum of normal  
CC - TISSUE SPECIFICITY: Restricted to the stratum granulosum/spinosum of psoriatic skin, and the  
skin, the stratum granulosum/spinosum of eccrine sweat glands. Low expression levels are  
CC found in the nasal cavity.  
CC - PTM: Substrate for transglutaminases. Acts as an acyl acceptor but  
CC not as an acyl donor.  
CC - SIMILARITY: Belongs to the cytatin family.  
CC -----  
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CC -----  
DR BMBL; U63800; AA065661; 1;  
DR EMBL; U81233; AA061305; 1; -.  
DR EMBL; BC011394; AAH31341; 1; -.  
DR HSMP; P01038; 1CW.  
DR HSP; P0147B; CS76.  
DR MM; 601891; -.  
DR GO; GO:0004859; P:cyteine protease inhibitor activity; TAS.  
DR GO:0000736; P:ambryogenesis and morphogenesis; TAS.  
DR SMART; SM00043; cystatin\_1.  
DR GO:0000010; cystatin.  
DR InterPro; IP000010; Cystatin.  
DR PROSITE; PS00287; Cystatin\_1.  
DR KIN Thio protease inhibitor; Signal; Glycoprotein.  
FT SIGNAL; 1 28 PROBABLE.  
FT CHAIN; 29 149 CYSTATIN M.  
FT ACT SITE 36 36 REACTIVE SITE.  
FT SITE 80 84 SECONDARY AREA OF CONTACT.  
FT DISULFID 98 113 BY SIMILARITY.  
FT DISULFID 126 146 BY SIMILARITY.  
FT CARBOHYD 137 137 137 N-LINKED (GLCNAC- -) (POTENTIAL).  
SQ SEQUENCE 149 AA; 16511 MW; 2076A ABFC9FAC8C CRC64;  
RESULT 14  
CYTC\_BOVIN STANDARD; PRT; 148 AA.  
ID CYTC\_BOVIN  
AC P01035;  
DT 21-JUL-1996 (Rel. 01, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cystatin C precursor (Colostrum thiol proteinase inhibitor).  
DN CS3  
OS Bos taurus (Bovine).  
OC Mamalia; Butharia; Cetartiodactyla; Craniata; Vertebrata; Euteleostomi;  
OC Bovidae; Bovines; Bos.  
NCI\_TaxID9913;

RN SEQUENCE FROM N.A.; SEQUENCE OF 66-83, AND CHARACTERIZATION.  
RP TISSUE=Cerebrospinal fluid, and Choroид plexus;

RX MEDLINE=90094199; PubMed=9434110;  
 RA Olsson S.-L., Ek B., Wilm M., Broborg G., Rask L., Björk I.;  
 RT Molecular cloning and N-terminal analysis of bovine cystatin C  
 RT Identification of a full-length N-terminal region.";  
 RL Biochim. Biophys. Acta 1343:203-210(1997).  
 RN [1]  
 RN SEQUENCE OF 37-146.  
 RX MEDLINE=85531205; PubMed=3891407;  
 RA Hirado M., Tsunawawa S., Sakiyama F., Niimobe M., Fujii S.;  
 PT "complete amino acid sequence of bovine colostrum low-Mr cysteine  
 proteinase inhibitor."  
 RT PROTEINS; PDB ID: 1BBS Latt. 186:141-45 (1985)  
 RL Latt. 186:141-45 (1985)  
 CC [-] FUNCTION: This is a thiol proteinase inhibitor.  
 CC [-] MASS SPECTROMETRY: MW=13420; METHOD=MALDI.  
 CC [-] SIMILARITY: Belongs to the cystatin family.  
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 DR HSMP; P01034; IG96.  
 DR InterPro; IPR00010; Cystatin.  
 DR Pfam; PF00031; cystatin\_1.  
 DR SMART; SM0043; CY\_1.  
 DR PROSITE; PS0028; CYSTATIN\_1.  
 DR DISULPID; Pyrocollone carboxylic acid.  
 KW Thiol protease inhibitor; Signal; Pyrocollone carboxylic acid.  
 PT SIGNAL 1 30 PROBABLE.  
 PT CHAIN 1 30 PROBABLE.  
 PT MOD\_RES 31 31 PYROCOLLINE CARBOXYLIC ACID (PROBABLE).  
 PT ACT\_SITE 40 40 REACTIVE SITE.  
 PT SITE 84 88 SECONDARY AREA OF CONTACT.  
 PT DISULPID 102 112 BY SIMILARITY.  
 PT DISULPID 126 146 BY SIMILARITY.  
 SQ SEQUENCE 148 AA; 16265 MM; BE40PB37CB9FOE CRC64!  
 Query Match 20.0%; Score 137.5; DB 1; Length 148;  
 Best Local Similarity 28.8%; Pred. No. 38-06; Gaps 4;  
 Matches 32; Conservative 25; Mismatches 35; Indels 19;  
 Gaps 4;  
 QY 24 NSPELEELTHITKLNAAENNATYFKIDNVTCKARYVACKKKPFDVARETTCSKESN 83  
 DB 48 NEEGVQALSLPAVSEBNRNSDNYAQSRVTRVIRAKQVVSMDNFIDVGRCTIK-S 105  
 QY 84 EPFTBSCC-----ETKLGQSUDCNAEAVYWPWEEKITPTVNHBCB 126  
 DB 106 QANLDSCPANOPHLKREKL---CSFQVTVPMKN---TINLVKESCO 147  
 RESULT 15  
 PDB\_RAT STANDARD PRT 378 AA.  
 ID PFB\_RAT  
 AC Q9Q79;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DB Pefuin-B precursor (IRL685).  
 GN PFB.  
 OS Rattus norvegicus (Rat).  
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prague-Dwalev; TISSUE=Liver;  
 RX MEDLINE=2040138; PubMed=1094975;  
 RA Olivier E., Soury E., Ruminy P., Husson A., Parmentier F., Daveau M.,  
 RA Saller J.-P.;  
 RT "Pefuin-B, a second member of the fetuin family in mammals."  
 Search completed: September 24, 2004, 14:09:13  
 Job time : 9.636 secs

Gencore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 24, 2004, 14:06:08 ; Search time 13.716 Seconds  
(without alignments)  
890.662 Million cell updates/sec

Title: US-10-661-784-3  
Perfect score: 687  
Sequence: 1 GSGKDFVQPPKICVGCPRD.....VPWBKRKIVPPVTVNHWBCEF 127

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: .283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing : Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_781\*  
1: Pir1\*  
2: Pir2\*  
3: Pir3\*  
4: Pir4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived from analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	618	90.0	427	1 KGHUJ1	kininogen, LMW pre-kininogen, LMW pre-kininogen, LMW I P
2	618	90.0	644	1 KGHDH1	kininogen, LMW pre-kininogen, LMW I P
3	440	64.0	436	1 KGBOL1	kininogen, LMW I P
4	440	64.0	621	1 KGBDH1	kininogen, LMW I P
5	413	60.1	434	1 KGBOL2	kininogen, LMW II
6	413	60.1	619	1 KGBDH2	K-kininogen, HMW II
7	410	59.7	433	2 A2B055	kininogen, HMW I
8	410	59.7	639	2 A25186	major acute phase T-kininogen, LMW I
9	388	56.5	430	2 B2B055	major acute phase T-kininogen, LMW I
10	388	56.5	430	2 KGRTM	major acute phase T-kininogen I prec
11	381	55.5	423	1 KGRTI	cystatin - bovine
12	380	55.3	430	1 UDHO	cystatin C precursors
13	137.5	20.0	112	1 UDHO	cystatin C precursors
14	132.5	19.3	146	1 UDHO	cystatin C precursors
15	130	18.9	127	2 S07085	cystatin C precursors
16	129	18.8	120	2 S10587	cystatin C - rat
17	128	18.6	111	2 A2B793	cystatin C - puff add
18	127.5	18.6	140	2 A36163	cystatin C precursors
19	124.5	18.1	141	2 B29632	cystatin SA precursor
20	118.5	17.2	139	1 UDCH	cystatin S precursors
21	113	16.4	141	2 J01470	cystatin S precursors
22	112	16.3	112	2 S68034	T-kininogen (clone)
23	112	16.3	91	2 S68035	T-kininogen (clone)
24	111	16.2	111	1 JC2040	cystatin - chum salmon
25	109.5	15.9	141	1 UDHP2	cystatin SN precursor
26	108.5	15.8	141	1 UDHP1	cystatin S precursor
27	107	15.6	139	1 T33740	hypothetical protein
28	106	15.4	132	2 JC4918	cystatin precursor
29	105.5	15.4	162	2 A43428	onchocystatin - ne

## ALIGNMENTS

RESULT 1

KGHUJ1  
Kininogen, LMW precursor [validated] - human  
N/Alternate name: alpha-2-thiol protease inhibitor; prokininogen  
N/Contains: bradykinin (Kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Homo sapiens (man)  
C/Date: 06-Jul-1982 #Sequence\_revision: 27-Nov-1985 #Text\_change: 08-Dec-2000  
C/Accession: A01800; B27699; A27800; A27801; A31905; T00752  
R/Ohkubo, I.; Kuwachi, K.; Takasawa, T.; Shiohawa, H.; Sasaki, M.  
Biochemistry 23, 5691-5697, 1984  
A/Title: Isolation of a human cDNA for alpha-2-thiol protease inhibitor and its iden!  
A/Reference number: A90490; MUID:5121621; PMID:6441591  
A/Accession: A01800  
A/Molecule type: mRNA  
A/Residues: 1-427 <C-terminal>  
A/Cross-references: GB:MI:1437; NID:9186751; PIDN:AA859551; 1; PID:9186853  
R/Lotzspeich, F.; Kellermann, J.; Henchen, A.; Raith, G.; Mueller-Esterl, W.  
R/Tagagaki, Y.; Kitamura, N.; Nakaniwa, S.  
J. Biol. Chem. 260, 8601-8609, 1985  
A/Title: Cloning and sequencing analysis of cDNAs for human high molecular weight and low  
A/Reference number: A92544; MUID:85234582; PMID:23989293  
A/Accession: B25376  
A/Molecule type: mRNA  
A/Residues: 1-427 <C-terminal>  
A/Cross-references: GB:MI:1437; NID:9186751; PIDN:AA859551; 1; PID:9186853  
R/Lotzspeich, F.; Kellermann, J.; Henchen, A.; Raith, G.; Mueller-Esterl, W.  
R/In King IV -> part A, Greenbaum, L.M. and Margoliash, H.S., eds., PP-91-35. Plenum, New York, 1982  
A/Title: Amino acid sequence of the light chain of human low molecular mass kininogen.  
A/Reference number: A27900  
A/Title: Cloning and sequencing analysis of cDNAs for human high molecular weight and low  
A/Reference number: A92544; MUID:85234582; PMID:23989293  
A/Molecule type: Protein  
A/Residues: 390-427 <C-terminal>  
R/Mindrotto, T.; Carrasco, O.A.; Proud, D.; Walz, D.; Scicli, A.G.  
Biochem. Biophys. Res. Commun. 155, 519-526, 1988  
A/Title: A new kinin moiety in human plasma kininogens.  
A/Reference number: A27699; MUID:88203021; PMID:3365237  
A/Accession: A276559  
A/Molecule type: Protein  
A/Residues: 380-399 <N-terminal>  
R/Maeda, H.; Matsumura, Y.; Kato, H.  
J. Biol. Chem. 263, 16051-16054, 1988  
A/Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic fluid  
A/Reference number: A31905; MUID:89034061; PMID:3162782  
A/Accession: A31905  
A/Molecule type: Protein  
A/Residues: 381-399 <N-terminal>  
R/Basaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.  
J. Biol. Chem. 263, 159-161, 1988  
A/Title: Identification of [hydroxyproline(3)-Lysyl]-bradykinin released from human platelets  
A/Reference number: A34030; MUID:88106632; PMID:33337729  
A/Accession: A34030  
A/Molecule type: Protein  
A/Residues: 380-389 <S-terminal>

R;Kitamura, N.;Kitagawa, H.;Fukushima, D.;Takagaki, Y.;Miyata, T.;Nakanishi, S.  
J.Biol.Chem.260:8610-8617,1985  
A;Title: Structure of the human kininogen gene and a model for its evolution  
A;Reference number: A9545; MUID:8534533; PMID:2982294

R;Annotations: gene organization  
R;Pierce, J.V.  
Ped. Proc. 27, 52-57, 1968  
A;Title: Structure of plasma kinins and kininogens.  
A;Reference number: A91455; MUID:9055622; PMID:4952632

C;Comment: The low molecular weight precursor is produced from the same gene as the HMW form (q)  
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the coagulation cascade, is a potent vasodilator, and is released from kininogen by kallikrein.  
C;Comment: Bradykinin residue is present in the kininogen prior to the release of bradykinin.

C;Genes:

A;Cross-references: GDB:1252561 OMIM:228960

A;Map position: 3q77-q27  
A;Inters: 65/3; 102/3; 111/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3  
C;Superfamily: kininogen; cystatin homology  
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glycine-rich domain; signal sequence  
P;1-16/Domain: Signal sequence #status predicted <SSG>  
P;19-127/Domain: Low molecular weight proteinogen (kininogen I) #status predicted <MAT>  
P;19-389/390-427/Domain: Low molecular weight product (kininogen II) #status predicted <Mat2>  
P;19-379/Domain: Low molecular weight heavy chain #status experimental <Bp1>  
P;142-253/Domain: cystatin homology <CV1>  
P;264-375/Domain: cystatin homology <CV3>  
P;380-389/Domain: bradykinin (kallikrein II) #status experimental <Bp2>  
P;381-389/Domain: bradykinin (kallikrein I) #status experimental <CV1>  
P;390-427/Domain: Low molecular weight light chain #status experimental <LCH>  
P;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
P;19/Modified site: pyrrolidone carboxylic acid (Gin) (in mature form) #status predicted  
P;48-169: 83-94, 107-126, 142-145, 205-218, 229-248, 264-267, 328-340, 351-370/Dissulfide bonds:  
P;48-169: 205-294/Binding site: carbohydrate (Asn) (covalent) #status predicted  
P;379-380/Cleavage site: Met-tys (kallikrein) #status experimental  
P;380-389/Modifited site: 4-hydroxyproline (Pro) (partial) #status experimental  
P;389-390/Cleavage site: Arg-ter (kallikrein) #status experimental  
P;401/Binding site: carbohydrate (Thr) (covalent) #status absent

Query Match score 618, DB 1, Length 427;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GRDFQPFKICVGRDPTNSPELEELTITKLNAAERNATYFKIDNYVKARQVV 62  
Db 253 GRDFQPFKICVGRDPTNSPELEELTITKLNAAERNATYFKIDNYVKARQVV 312

Qy 63 AGKRYFIDPVARETTGCKESEETKQGSDCAEVTVPKKLYPTV 118  
Db 313 AGKRYFIDPVARETTGCKESEETKQGSDCAEVTVPKKLYPTV 368

**RESULT 2**

KH01  
Kininogen. HMW precursor [validated] - human  
N;Alternate name: alpha-2-thiol proteinase inhibitor, proproteinase prokininogen  
N;Contracted name: kallikrein (kallikrein I), HMW kininogen I; HMW kininogen  
C;Species: Homo sapiens (human)  
C;Date: 28-May-1986 #sequence revision 08-Dec-2000  
C;Accession: A01279; A2576; S3222; A91153; A24871; A27639; A31905; A34030; S02  
R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.  
Biochemistry 23: 5691-5697, 1984  
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identification  
A;Reference number: A90490; MUID:85122621; PMID:6141591

A;Cross-references: 1-369 <ORK>  
A;Molecular type: mRNA  
A;Accession: A01279

A;Cross-references: GB:KO2566; NID:917889  
A;Molecular type: Protein  
A;Experimental source: urine  
A;Note: this peptide had Pro-383 modified to 4-hydroxyproline

J.Biol.Chem. 260: 8601-8609, 1985  
A;Title: Cloning and analysis of cDNAs for human high molecular weight and low molecular weight kininogens  
A;Reference number: A92544; MUID:2989293  
A;Accession: A25276

A;Molecule type: mRNA  
A;Residues: 1-369 <ORK>  
A;Accession: A01279

A;Molecule type: mRNA  
A;Residues: 1-369 <ORK>  
A;Accession: A01279

A;Molecule type: protein  
A;Residues: 380-389 <KAR1>  
A;Experimental source: urine  
A;Accession: B61495  
A;Molecule type: protein  
A;Residues: 381-389 <KAR2>

A;Molecule type: protein  
A;Residues: 380-389 <MIN>  
A;Accession: A31905

A;Molecule type: protein  
A;Residues: 381-389 <KAR1>  
R;Saaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.  
Biochem. Biophys. Res. Commun. 152: 519-526, 1988  
A;Title: Identification of hydroxypyrolyl(3)-hydroxypyroline(3)-hydroxypyrolyl(3)-bradykinin released from human plasma  
A;Reference number: A34030; MUID:88205021; PMID:3165237

A;Molecule type: protein  
A;Residues: 380-389 <MIN>  
A;Accession: A31905; MUID:89034061; PMID:3182782

A;Molecule type: protein  
A;Residues: 381-389 <KAR1>  
J.Biol.Chem. 253: 16051-16054, 1988  
A;Title: Purification and identification of hydroxypyrolyl(3)-bradykinin in ascitic fluid  
A;Reference number: A37639; MUID:88205021; PMID:3165237

A;Molecule type: protein  
A;Accession: A31905; MUID:89034061; PMID:3182782

A;Molecule type: protein  
A;Accession: A31905; MUID:89034061; PMID:3182782

A;Molecule type: protein  
A;Accession: A31905; MUID:89034061; PMID:3182782

R;Lenarcic, B.; Gabriljevic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.  
Biol.Chem. Hoppe-Seyler 369: 257-261, 1988  
A;Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in inflammatory and  
A;Reference number: S02482; MUID:89016517; PMID:3264507

A;Molecule type: protein  
A;Accession: S02482  
A;Residues: 1-19-189-192-310-314-381-389 <LEN1>  
R;Kato, H.; Matsumura, Y.; Maeda, H.  
FEBS Lett. 232: 252-254, 1988  
A;Title: Isolation and identification of hydroxypyroline analogues of bradykinin in human plasma  
A;Reference number: A61495; MUID:188211869; PMID:3337729

A: Experimental source: urine  
 A: Note: this peptide had Pro-383 modified to 4-hydroxyproline  
 A: Molecule type: protein  
 A: Accession: 380-389 <KAT>  
 R: Lenarcic, B.; Krasovec, M.; Ritossa, A.; Olafsson, I.; Turk, V.  
 PDB Locr: 280, 211-215, 1991  
 A:Title: Inactivation of human cystatin C and kininogen by human cathepsin D.  
 A: Reference number: S14303; MUID:91192133; PMID:12013314

A: Molecule type: protein  
 A: Residues: 64-355,'N',351-375 <LEN2>  
 Biochem. J. 307, 341-346, 1995  
 A:Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity  
 A: Reference number: 555219; MUID:95251593; PMID:7733867

A: Molecule type: Protein  
 A: Residues: 450-452,'X',454,'X',456 <LIT>  
 R: Straczek, J.; Maachi, F.; Le Nguyen, D.; Beccchi, M.; Heulin, M.H.; Nabet, P.; Belleville, P.; PDB Locr: 373, 207-211, 1993  
 A:Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor-I receptor activity  
 A: Reference number: 868059; MUID:96033974; PMID:7589467

A: Molecule type: protein  
 A: Residues: 431-434 <STR>  
 R: Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takegaki, Y.; Miyata, T.; Nakaniishi, S.  
 J. Biol. Chem. 260, 8610-8617, 1985  
 A:Title: Structural organization of the human kininogen gene and a model for its evolution  
 A: Reference number: A9551; MUID:8524583; PMID:2889294

A: Comments: annotation; gene organization  
 R:Pierce, J.V.  
 Fed. Proc. 27, 52-57, 1968  
 A:Title: Structural features of plasma kinins and kininogens.  
 A: Reference number: A91155; MUID:90255622; PMID:4952632

C:Comments: annotation; bradykinin  
 C:Comment: The hMW kininogen precursor and the LMW form are produced from the same gene  
 C:Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the hMW kininogen light chain is important for the biological activity of hMW kininogen.  
 C:Comment: Glycine/histidine/lysine-rich region of hMW kininogen, released from bradykinin, is a potent vasodilator.  
 C:Comment: Bradykinin, released from kininogen by kallikrein, is present in the kininogen prior to the release of bradykinin.  
 C:Genetics:  
 A:Map Position: 3Q21-3Q27  
 A:Cross-references: GDB:125256; OMIM:228960

A:Intron: 65/3; 102/3; 131/1; 186/3; 224/3; 253/1; 310/3; 346/3; 375/3  
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl  
 P:1-18/Domain: signal sequence #status experimental <SIG>  
 P:19-379/390-644/Domain: hMW kininogen I (prokininogen) #status experimental <MATI>  
 P:19-379/390-644/Domain: hMW kininogen II #status experimental <MAT2>  
 P:19-1131/Domain: hMW kininogen heavy chain #status experimental <HCH>  
 P:1-12/253/Domain: cystatin homology <C1>  
 P:264-375/Domain: cystatin homology <CY3>  
 P:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>  
 P:380-644/Domain: hMW kininogen light chain #status experimental <BDY>  
 P:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats  
 P:421-434/Product: low molecular weight growth promoting factor #status experimental <GFBH>  
 P:28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:  
 P:48/Binding site: pyroglutamyl carboxylic acid (Gln) (In nature form) #status experimental  
 P:159,205,29/Binding site: carbohydrate (Asn) (covalent) #status absent  
 P:339-380/Cleavage site: carbohydride (Asn) (covalent) #status experimental  
 P:333/Modified site: 4-hydroxyproline (pro) (partial) #status experimental  
 P:319-390/Cleavage site: carbohydride (Asn) (covalent) #status experimental  
 P:401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 P:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match score: 618; DB: 1; Length: 644;  
 Best Local Similarity: 100.0%; Pred. No.: 5.7e-50;  
 Matches: 116; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

A:Experimental source: urine  
 A:Note: this peptide had Pro-383 modified to 4-hydroxyproline  
 A: Molecule type: protein  
 A: Accession: C61495  
 A: Alternate name: protein  
 A: Residues: 380-389 <KAT>  
 R: Lenarcic, B.; Krasovec, M.; Ritossa, A.; Olafsson, I.; Turk, V.  
 PDB Locr: 280, 211-215, 1991  
 A:Title: Inactivation of human cystatin C and kininogen by human cathepsin D.  
 A: Reference number: S14303; MUID:91192133; PMID:12013314

A: Molecule type: protein  
 A: Residues: 64-355,'N',351-375 <LEN2>  
 Biochem. J. 307, 341-346, 1995  
 A:Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity  
 A: Reference number: 555219; MUID:95251593; PMID:7733867

A: Molecule type: Protein  
 A: Residues: 450-452,'X',454,'X',456 <LIT>  
 R: Straczek, J.; Maachi, F.; Le Nguyen, D.; Beccchi, M.; Heulin, M.H.; Nabet, P.; Belleville, P.; PDB Locr: 373, 207-211, 1993  
 A:Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor-I receptor activity  
 A: Reference number: 868059; MUID:96033974; PMID:7589467

A: Molecule type: protein  
 A: Residues: 431-434 <STR>  
 R: Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takegaki, Y.; Miyata, T.; Nakaniishi, S.  
 J. Biol. Chem. 260, 8610-8617, 1985  
 A:Title: Structural organization of the human kininogen gene and a model for its evolution  
 A: Reference number: A9551; MUID:8524583; PMID:2889294

A: Comments: annotation; gene organization  
 R:Pierce, J.V.  
 Fed. Proc. 27, 52-57, 1968  
 A:Title: Structural features of plasma kinins and kininogens.  
 A: Reference number: A91155; MUID:90255622; PMID:4952632

C:Comments: annotation; bradykinin  
 C:Comment: The hMW kininogen precursor and the LMW form are produced from the same gene  
 C:Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the hMW kininogen light chain is important for the biological activity of hMW kininogen.  
 C:Comment: Glycine/histidine/lysine-rich region of hMW kininogen, released from bradykinin, is a potent vasodilator.  
 C:Comment: Bradykinin, released from kininogen by kallikrein, is present in the kininogen prior to the release of bradykinin.  
 C:Genetics:  
 A:Map Position: 3Q21-3Q27  
 A:Cross-references: GDB:125256; OMIM:228960

A:Intron: 65/3; 102/3; 131/1; 186/3; 224/3; 253/1; 310/3; 346/3; 375/3  
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl  
 P:1-18/Domain: signal sequence #status experimental <SIG>  
 P:19-379/390-644/Domain: hMW kininogen I (prokininogen) #status experimental <MATI>  
 P:19-379/390-644/Domain: hMW kininogen II #status experimental <MAT2>  
 P:19-1131/Domain: hMW kininogen heavy chain #status experimental <HCH>  
 P:1-12/253/Domain: cystatin homology <C1>  
 P:264-375/Domain: cystatin homology <CY3>  
 P:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>  
 P:380-644/Domain: hMW kininogen light chain #status experimental <BDY>  
 P:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats  
 P:421-434/Product: low molecular weight growth promoting factor #status experimental <GFBH>  
 P:28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:  
 P:48/Binding site: carbohydrate (Asn) (covalent) #status absent  
 P:159,205,29/Binding site: carbohydride (Asn) (covalent) #status experimental  
 P:339-380/Cleavage site: carbohydride (Asn) (covalent) #status experimental  
 P:333/Modified site: 4-hydroxyproline (pro) (partial) #status experimental  
 P:319-390/Cleavage site: carbohydride (Asn) (covalent) #status experimental  
 P:401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 P:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match score: 618; DB: 1; Length: 644;  
 Best Local Similarity: 100.0%; Pred. No.: 5.7e-50;  
 Matches: 116; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

RESULT 3  
 KGBOJ1  
 Kininogen, LMW I precursor - bovine  
 N:Alternate name: alpha-2-thiol proteinase inhibitor; preprokininogen  
 N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 22-Jun-1999  
 C:Accession: A01283  
 R:Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakaniishi, S.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983  
 A:Title: Primary structures of bovine liver low molecular weight kininogen precursors  
 A:Reference number: A93984; MUID:83117859; PMID:6372010  
 A:Accession: A01283  
 A/Molecule type: mRNA  
 A/Residues: 1-436 <NM>  
 A/Cross-references: GB:J00010; GB:V00426; PID:9163256; PID:9163257  
 C:Comment: The LMW kininogen precursor is produced from the same gene as the hMW form  
 C:Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the hMW form  
 C:Comment: Bradykinin, released from kininogen prior to the release of bradykinin.  
 C:Superfamily: kininogen; cyatatin homology  
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; SIG; P19-436/Product: LMW kininogen I heavy chain #status predicted <MAT>  
 P:19-378/Product: LMW kininogen I heavy chain #status predicted <HCH>  
 P:19-130/Domain: cystatin homology <C1>  
 P:141-252/Domain: cystatin homology <C2>  
 P:263-374/Domain: cystatin homology <CY3>  
 P:379-388/Product: lysyl-bradykinin (kallidin II) #status predicted <KBDY>  
 P:380-388/Product: bradykinin (kallidin II) #status predicted <BDY>  
 P:389-436/Product: pyroglutamyl carboxylic acid (Gln) (In nature form) #status predicted <GFBH>  
 P:389-436/Modified site: pyroglutamyl carboxylic acid (Gln) (In nature form) #status predicted <GFBH>  
 P:27-40,82-33,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond  
 P:47,97,168,169,197,204/Binding site: carbohydrate (Asn) (covalent) #status predicted <GFBH>  
 P:378-379/Cleavage site: Met-Lys (kallikrein) #status Predicted  
 P:382/Modified site: 4-hydroxyproline (Pro) #status Predicted  
 P:388-389/Cleavage site: Arg-Ser (kallikrein) #status Predicted  
 Query Match score: 618; DB: 1; Length: 436;  
 Best Local Similarity: 70.4%; Pred. No.: 1.7e-31;  
 Matches: 81; Conservative: 14; Mismatches: 20; Indels: 0; Gaps: 0;

RESULT 4  
 KGBOH1  
 Kininogen, HMW I precursor - bovine  
 N:Alternate name: alpha-2-thiol proteinase inhibitor; preprokininogen  
 N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 22-Jun-1999  
 C:Accession: A01283; A91938; A95559  
 R:Kitamura, N.; Takegaki, Y.; Furuno, S.; Tanaka, T.; Nawa, H.; Nakaniishi, S.  
 Natur. 305, 545-549, 1983  
 A:Title: A single gene for bovine high molecular weight and low molecular weight kininogen  
 A:Reference number: A93317; MUID:8014106; PMID:6571699

A;Accession: A01281  
 A;Molecule type: mRNA  
 A;Residues: 1-621 <KIT>  
 A;Cross-references: GB:V01491; GB:K01757; NID:9491; PID:CAA24735.1; PID:9492  
 R;Kato, H.; Nagasawa, S.; Suzuki, T.  
 J. Biochem. 67, 311-323, 1970  
 A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and  
 A;Reference number: A91923; MUID:70180420; PMID:4986212  
 A;Accession: A91923  
 A;Molecule type: protein  
 A;Residues: 378-393 <HAN>  
 R;Suayoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Miyata, T.; Iwanaga,  
 J. Biol. Chem. 262, 2768-2779, 1987  
 A;Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of C  
 A;Reference number: A91938; MUID:87137330; PMID:3546295  
 A;Accession: A91938  
 A;Molecule type: protein  
 A;Residues: 2'-20123-'I', 125-127-'I', 129-378 <SUE>  
 R;Lorrespeich, F.; Kellermann, J.; Henschen, A.; Poertsch, B.; Muller-Esserl, W.  
 Eur. J. Biochem. 155, 307-314, 1985  
 A;Title: The amino acid sequence of the light chain of human high-molecular-mass kininoc  
 A;Reference number: A91153; MUID:86030270; PMID:4054110  
 A;Contents: annotation: bovine cleavage sites; bovine carbohydrate binding sites  
 R;Suayoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.;  
 Seikagaku 56, 808, 1984  
 A;Title: Disulfide bonds in bovine HMW kininogens.  
 A;Contents: annotation: disulfide bonds  
 A;Note: article in Japanese  
 C;Comment: The raw kininogen precursor is produced from the same gene as the LMW form as a cysteine protease inhibitor, takes part in initiation of the coagulation cascade.  
 C;Comment: The Glycine/histidine/lysine-rich region of HMW kininogen light chain is important for the release of bradykinin, a potent vasodilator.  
 C;Superfamily: Kininogen; cystatin homology  
 C;Keywords: alternative splicing; blood coagulation; cysteine protease inhibitor; disulfide bond; signal sequence; status predicted; SIG;  
 P:1-18/Domain: signal sequence #status predicted <SIG>  
 P:19-621/Product: HMW kininogen I #status predicted <HAN>  
 P:19-379/Domain: cystatin homology <CV1>  
 P:141-252/Domain: cystatin homology <CV2>  
 P:263-377/Domain: cystatin homology <CV3>  
 P:379-388/Product: bradykinin (kallikrein) (kallidin I) #status experimental <KBDS>  
 P:389-462/Product: HMW kininogen I light chain #status experimental <B9Y>  
 P:417-488/Region: glycine/histidine/lysine-rich  
 P:19/Modified site: pyrolysis carbonylic acid (Gln) (in mature form) #status experimental  
 P:87-168,169-204/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 P:87-168,169-204/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental  
 P:197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
 P:378-379/Cleavage site: Met-(ys) (kallikrein) #status experimental  
 P:182/Modified site: 4-hydroxyproline (Pro) #status predicted  
 P:388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental  
 P:198-406,512/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 P:98-499/Cleavage site: Arg-Thr (kallikrein) #status experimental  
 Query Match Score 440, DB 1, Length 621;  
 Best Local Similarity 70.4%, Pred. No. 2.4e-33;  
 Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 64 GKKRKYFDPVARETCSKESNEELTSCETKLGQDCAEVYVPPWEKKIYPTV 118  
 Db 313 GLKRYKIVPARETCSKGSNEELTSCETKLGQDCAEVYVPPWEKKIYPTV 367

RESULT 5  
 KB012  
 Kininogen, LMW II precursor - bovine  
 N;Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen  
 N;Contains: bradykinin (kallikrein); kininogen I; kininogen II; prokininogen  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 28-May-1999  
 C;Accession: A01284  
 R;Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 90-93, 1983  
 A;Title: Primary structures of bovine liver low molecular weight kininogen precursors a  
 A;Reference number: A91984; MUID:83117859; PMID:6572010  
 A;Accession: A01284  
 A;Molecule type: mRNA  
 A;Residues: 1-434 <NAW>  
 A;Cross-references: GB:V0047; GB:J00011; NID:9489; PID:CAA23710.1; PID:9490  
 C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the HMW form of bradykinin, released from kininogen by kallikrein, is a potent vasodilator, Xproline residue is present in the kininogen prior to the release of bradykinin.  
 C;Superfamily: Kininogen; cystatin homology  
 C;Keywords: alternative splicing; blood coagulation; cysteine protease inhibitor; gly-  
 P:1-18/Domain: signal sequence #status predicted <SIG>  
 P:19-34/Product: LMW kininogen II #status predicted <HAT>  
 P:19-377/Domain: LMW kininogen I heavy chain #status predicted <HCH>  
 P:19-130/Domain: cystatin homology <CV1>  
 P:261-372/Domain: cystatin homology <CV2>  
 P:377-386/Product: bradykinin (kallidin I) #status predicted <KBDS>  
 P:378-434/Product: LMW kininogen I light chain #status predicted <B9Y>  
 P:119/Modified site: pyrolysis carbonylic acid (Gln) (in mature form) #status predicted  
 P:27-404,82-91,106-125,111-144,205-217,228-247,261-264,325-337,348-367 #disulfide bonds:  
 P:47, 87, 169, 197, 204, 280/Binding site: carboxydrate (Asn) (covalent) #status predicted  
 P:376-377/Cleavage site: Met-(ys) (kallikrein) #status predicted  
 P:380/Modified site: 4-hydroxyproline (Pro) #status predicted  
 P:386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted

Query Match Score 60.1%; Score 413; DB 1; Length 434;  
 Best Local Similarity 67.2%; Pred. No. 5.5e-31; Mismatches 22; Indels 2; Gaps 1;

Qy 3 GKDPRQQPTKICUGCPGRDIFTNSPELSELTATITKLNAAENATPYPKIDNVVKARVQYV 62  
 Db 252 GEDFL--PPMVCGVKPKPVPVDSPELPEALNSIAKLNAAHDGFTYFKIDTVKATVQYV 309

Qy 63 AGKRYFDPVARETCSKESNEELTSCETKLGQDCAEVYVPPWEKKIYPTV 118  
 Db 310 GGKRYKIVPARETCSKGSNEELTSCETKLGQDCAEVYVPPWEKKIYPTV 365

RESULT 6  
 KB012  
 Kininogen, HMW II precursor - bovine  
 N;Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen  
 N;Contains: bradykinin (kallikrein); kininogen I; kininogen II; prokininogen  
 C;Species: Bos primigenius taurus (cattle)  
 C;Accession: A01282; A91923; A91941; A91938; B29559  
 R;Kitamura, N.; Takigaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.  
 A;Title: A single gene for bovine high molecular weight and low molecular weight kininogen  
 A;Reference number: A93317; MUID:8401406; PMID:6571639  
 A;Accession: A01282  
 A;Molecule type: mRNA  
 A;Residues: 1-619 <KIT>  
 A;Cross-references: GB:V01492; NID:9493; PID:CAA24736.1; PID:9494  
 R;Kato, H.; Nagasawa, S.; Suzuki, T.

Qy 4 KDFVQPTKICUGCPGRDIFTNSPELSELTATITKLNAAENATPYPKIDNVVKARVQYV 63  
 Db 253 KDFVQSPTRLCAGCBKPKIPDVSPDPLREPLSHIAEHDGFTVKGATVQYV 312

J. Biochem. 67, 313-323, 1970 A/Tittle: Studies on the structure of bovine kininogen; cleavages of disulfide bonds and A/Reference number: A91923; MUID:70180420; PMID:4986212	Qy 3 GKDPPQPTKICGGCPDIPNSPELEETLTITKNAENNATTPYKIDNPKARVQVV 62 Db 252 GEPL--PPNVCVGCPKP/PVDPDPLEALHNSIAKINAHBDGTYPKIDTVKAVV 309	
A/Molecule type: Protein A/Residues: 376-391 <Xaa> R/Han, Y.N., Kato, H., Iwanaga, S., Suzuki, T. J. Biochem. 79, 1201-1222, 1976 A/Tittle: Primary structure of bovine plasma high-molecular-weight kininogen. The amino acid sequence number: A91941; MUID:76260155; PMID:956151	Qy 63 AGKRYFIDPVARETCSKESNEELTESCETKLGQSLODCNAEVYVPPWEEKIYPTV 118 Db 310 GGKYSIVPIARETCSKESNEELTSKSCBINHQILCDANVYVPPWEEKIYPTV 365	
A/Molecule type: Protein A/Residues: 456-496 <Xaa> R/Sueyoshi, T., Miyata, H., Hashimoto, N., Kato, H., Hayashida, H., Iwanaga, S. J. Biol. Chem. 262, 2768-2779, 1987 A/Tittle: Bovine high molecular weight kininogen. The amino acid sequence, positions of C-terminal amidation and the primary structure of bovine high-molecular-weight kininogen. Ami A/Reference number: A92627; MUID:8717530; PMID:3146295	RESULT 7 A/Accession: A92627 A/Molecule type: Protein A/Residues: 210-104, 'B', 106-255, 'XX', 257-376 <SUB> R/Lotterpeich, P., Kallermann, J., Henschien, A., Feiertach, B., Muller-Bateri, W. Eur. J. Biochem. 152, 307-314, 1985 A/Tittle: The bovine acid sequence of the light chain of human high-molecular-mass kininog A/Reference number: A91153; MUID:16030270; PMID:4054110 A/Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R/Sueyoshi, T., Miyata, H., Kato, H., Iwanaga, S. Seikagaku 56, 89, 1984 A/Tittle: Disulfide bonds in bovine HMW kininogens. A/Reference number: A94300 A/Contents: annotation; disulfide bonds A/Note: article in Japanese	Qy 3 GKDPPQPTKICGGCPDIPNSPELEETLTITKNAENNATTPYKIDNPKARVQVV 62 Db 253 GDDLFELLSPDGPGPANIPVDSPELKEALGHSAQLNAENHTTPYKIDTVKAKTSQVV 312
C/Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as a single polypeptide chain. The HMW kininogen light chain, which part in initiation of the coagulation cascade, is released from kininogen by kallikrein, a potent vasodilator, and xyproline residue is present in the kininogen prior to the release of bradykinin. C/Superfamily: Kininogen; cystatin homology C/Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl P:1/9-619/Product: HMW kininogen II #status predicted <SIG> P:1/9-376/Product: HMW kininogen II #status experimental <HCH> P:1/9-130/Region: glycine/histidine/lysine-rich P:1/11-232/Domain: cystatin homology <CY1> P:2/21-372/Domain: cystatin homology <CY2> P:3/17-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY> P:3/18-386/Product: bradykinin (kallidin I) #status experimental <BDY> P:3/8-619/Product: HMW kininogen II #status experimental <LCH> P:4/8-488/Region: glycine/histidine/lysine-rich P:4/9-488/Region: glycine/histidine/lysine-rich P:2/37-377/Cleavage site: carboxylic acid (Gln) (In mature form) #status experiment P:2/37-377/Cleavage site: carboxylate (Asn) (covalent) #status absent P:3/8-387/Cleavage site: 4-hydroxyproline (Pro) #status predicted P:3/95-400,404,510/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental P:3/9,39,516,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status ex P:4/9-497/Cleavage site: Arg-Thr (kallikrein) #status experimental	Query Match Score 410; DB 2; Length 639, Best Local Similarity 66.4%; Pred. No. 1..66-30; Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;	

**Db** 253 GDDLFELLPEPDCPGCPNIPVDSPELKEALGHSAQQLAENNNHTFPKIDTVKTKTQSQQV 312  
**Qy** 63 AGKRTFIDPVARETCSKESNEBLTSCSTKCGSLSLDNARYVYVWPKIYPTV 118  
**Db** 313 AGKTYVIEPIARSTKCGSKESNEBLTADCTKLGQSLNANCNANVMPWENKVYPTV 368

**RESULT 9**  
**A23897**  
 major acute phase alpha-1 protein (version 2) - rat  
*C;Species: Rattus norvegicus (Norway rat)*  
*C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 20-Aug-1999*  
**R;Anderson, K.P.; Heath, P.C.**  
**J; Biol. Chem. 260, 12065-12071, 1985**  
**A;Reference number: A23897; MUID:86008266; PMID:2413019**  
**A;Molecule type: Protein**  
**A;Residues: 1-14 <AND1>**  
**A;Accession: B23897**  
**A;Molecule type: mRNA**  
**A;Residues: 5-430 <AND2>**  
**A;Cross-references: GB:M11661; NID:R030307; PIDN:AAA41570.1; PMID:9205308**  
**A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415**  
*C;Superfamily: kininogen cystatin homology*  
*P;19-130/Domain: cystatin homology <CY1>*  
*P;141-252/Domain: cystatin homology <CY2>*  
*P;263-374/Domain: cystatin homology <CY3>*

**Query Match** 56.5% Score 388; DB 2; Length 430;  
**Best Local Similarity** 62.1%; **Pred. No.** 1.2e-28;  
**Matches** 72; **Conservative** 15; **Mismatches** 29; **Indels** 0; **Gaps** 0;

**Qy** 3 GDDLFELLPEPDCPGCPNIPVDSPELKEALGHSAQQLAENNNHTFPKIDTVKTKTQSQQV 62  
**Db** 252 GDDLFELLPEPDCPGCPNIPVDSPELKEALGHSAQQLAENNNHTFPKIDTVKTKTQSQQV 311

**Qy** 63 AGKTYVIEPIARSTKCGSKESNEBLTSCSTKCGSLSLDNACYVYVWPKIYPTV 118  
**Db** 312 AGKTYVIEPIARSTKCGSKESNEBLTADCTKLGQSLNANCNANVMPWENKVYPTV 367

**RESULT 11**  
**KGRTM**  
 major acute phase alpha-1 protein precursor - rat (fragment)  
*C;Keywords: bradykinin*  
*C;Species: Rattus norvegicus (Norway rat)*  
*C;Date: 27-Nov-1985 #text\_change 12-Apr-1996*  
*C;Sequence\_revision 27-Nov-1985*  
*C;Accession: A01285*  
*R;Cole, T.; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.*  
*A;Title: Major acute phase alpha-protein of the rat is homologous to bovine kininogen at A1285*  
*A;Reference number: A01285; MUID:85127561; PMID:2578992*  
*A;Molecule type: mRNA*  
*A;Residues: 1-423 <COL>*  
*C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflammation it is converted to bradykinin by cysteine proteinase inhibitor/duplication, glycoprotein, inflammatory mediator.*

**Query Match** 55.5% Score 361; DB 1; Length 423;  
**Best Local Similarity** 62.1%; **Pred. No.** 5.3e-28;  
**Matches** 72; **Conservative** 14; **Mismatches** 0; **Indels** 0; **Gaps** 0;

**Qy** 3 GDDLFELLPEPDCPGCPNIPVDSPELKEALGHSAQQLAENNNHTFPKIDTVKTKTQSQQV 62  
**Db** 245 GDDLFELLPEPDCPGCPNIPVDSPELKEALGHSAQQLAENNNHTFPKIDTVKTKTQSQQV 304

**Qy** 63 AGKTYVIEPIARSTKCGSKESNEBLTSCSTKCGSLSLDNACYVYVWPKIYPTV 118  
**Db** 305 AGKTYVIEPIARSTKCGSKESNEBLTSCSTKCGSLSLDNACYVYVWPKIYPTV 160

**RESULT 12**  
**KGRTM**  
 T-kininogen I precursor - rat  
*N;Reference number: B2855*  
*N;Species: Rattus norvegicus (Norway rat)*  
*N;Accession: B2855*  
*N;Molecule type: protein*  
*A;Residues: 'E',20-28,'WD','28-48',376-430 <ENJ>*  
*A;Accession: C25226*  
*A;Molecule type: Protein*

**Db** 263 AGKTYVIEPIARSTKCGSKESNEBLTSCSTKCGSLSLDNACYVYVWPKIYPTV 160

**RESULT 13**  
**T-kininogen I precursor - rat**  
*N;Reference number: A01286*  
*N;Species: Rattus norvegicus (Norway rat)*  
*N;Accession: A01286*  
*N;Molecule type: protein*  
*A;Residues: 'E',20-28,'WD','28-48',376-430 <ENJ>*  
*A;Accession: A20526*  
*A;Molecule type: Protein*

R./Purito-Kato, S./ Matsumoto, A./ Kitamura, N./ Nakaniishi, S.  
J. Biol. Chem. 260, 12054-12059, 1985  
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.  
A:Reference number: A92496 / MUID:86008264; PMID:2413018  
A:Accession: A01286  
A:Molecule type: mRNA  
A:Residues: 1-130 <PUR>  
A:Cross-references: GB:MM11833; NID:G205084; PID:AAA1489\_1; PID:9205085  
R.Kitamura, H.; Kitamura, N.; Hayashi, H.; Miyata, T.; Nakaniishi, S.  
J. Biol. Chem. 262, 2190-2198, 1987  
A:Title: Differing expression patterns and evolution of the rat kininogen gene family.  
A:Reference number: A92625; MUID:87117443; PMID:3029068  
A:Accession: D24486  
A:Molecule type: DNA  
A:Residues: 375-430 <KIT>  
R. Enjiochi, K.; Yato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.  
J. Biol. Chem. 263, 973-979, 1988  
A:Title: Purification and characterization of rat T-kininogens isolated from plasma of a  
A:Reference number: A92729; MUID:88087226; PMID:3121623  
A:Accession: A25226  
A:Molecule type: protein  
A:Residues: 'B'-20-'B'-316-'B'-410 <ENJ>  
R.Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.  
Jpn. J. Cancer Res. 81, 63-68, 1990  
A:Title: Identification of a protein increasing in serum of Nagase analbuminemic rats by  
A:Reference number: PL0193; PMID:2108948  
A:Accession: PL0193  
A:Residues: 330-420, 'R', 422-429, 'P' <KAN>  
R.Anderson, K.P.; Croyle, M.L.; Lingel, J.B.  
J. Biol. Chem. 262, 2345-2351, 1987  
A:Title: Primary structure of a gene encoding rat T-kininogen.  
A:Reference number: JQ00377; MUID:90034173; PMID:2806908  
A:Accession: JQ0027  
A:Molecule type: mRNA  
A:Residues: 1-66; 'B', 62-113, 'R', 115-165, 'P', 167-178, 'TKI', 182-211, 'P', 213-256, 'S', 258-38  
A:Experimental source: strain Sprague-Dawley  
A:Keywords: R.; Kitamura, N.; Ohkubo, H.; Nakaniishi, S.  
R.Kagiyama, R.; Kitamura, N.; Ohkubo, H.; Nakaniishi, S.  
J. Biol. Chem. 262, 2345-2351, 1987  
A:Title: Differing utilization of homologous transcription initiation sites of rat K and  
A:Reference number: A25488; PMID:87137465; PMID:3818598  
A:Accession: B23488  
A:Statistical: preliminary  
A:Molecular type: DNA  
A:Residues: 1-48, <KAG>  
R.Enjiochi, K.; Yato, H.; Hayashi, I.; Ohishi, S.; Iwanaga, S.  
J. Biol. Chem. 263, 965-972, 1988  
A:Title: Purification and characterization of two kinds of low molecular weight kininogen  
A:Reference number: A28525; MUID:88087225; PMID:3335530  
A:Accession: A28525  
A:Molecule type: protein  
A:Residues: 376-410 <EN2>  
R.Serra, F.; Walter, R.; Vautravers, P.; Guiguz, Y.  
Arch. Biochem. Biophys. 322, 333-338, 1995  
A:Title: Identification of several isoforms of LMW kininogen expressed in the liver of agouti  
A:Reference number: S68034; MUID:36033652; PMID:7574705  
A:Molecule type: mRNA  
A:Residues: 340-410 <S1B>  
A:Experimental source: clone DSG17  
C:Comment: At least three types of LMW kininogen precursors are present in rat plasma,  
ceding bradykinin.  
C:Comment: T-kininogens contain T-kinin (1-S-bradykinin), a novel kinin isolated after  
d of an Arg or Lys. It is probably not released from its precursor by either tissue or  
C:Comment: The T-kininogens are produced in response to an inflammatory stimulant.  
C:Comment: The T-kininogens are produced in response to an inflammatory stimulant.  
C:Genetics: 65/3, 102/3, 130/1, 187/3, 223/2, 252/1, 309/3, 345/3, 374/3, 398/3  
C:Superfamily: kininogen; cystatin homology  
C:Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glycopro-  
F:1-18/Domain: signal sequence predicted <SIG>  
F:19-430/Product: T-kininogen 1 #statin 1 #statin experimental <NAT>

P:19-130/Domain: cystatin homology <CY1>  
P:141-322/Domain: cystatin homology <CY2>  
P:263-374/Domain: cystatin homology  
P:318-366/Product: bradykinin #status Predicted <BDY>  
P:119/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experiment  
P:8/124,162,204,322/Binding Site: carbohydrate (Asn) (covalent) #status Predicted  
P:8/94,107-125,141-144,205-217,228-47,327-339,350-365/Disulfide bonds: #scatcu  
Query Match Score 380; DB 1; Length 430;  
Best Local Similarity 62.1%; Pred. No. 678-28;  
Matches 14; Mismatches 30; Indels 0; Gaps 0;  
Conservative 14; N/A  
72; C:Species: Bos primigenius taurus (cattle)  
C:Accession: A01271  
C:Accession: A01271  
R.Hirada, M.; Imanawa, S.; Sakiyama, F.; Minobe, M.; Fujii, S.  
PEBS Lett. 186, 41-45, 1985  
A:Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase  
A:Reference number: A01271; MUID:85231205; PMID:3891407  
A:Accession: A01271  
A:Molecule type: Protein  
A:Residues: 1-112 <HHR>  
C:Superfamily: cystatin, cysteatin homology  
C:Keywords: cysteatin; cysteine proteinase inhibitor  
P:2-112/Domain: cystatin homology <CRY>  
P:48-52/Region: inhibitory #status Predicted  
P:66-76,90-110/disulfide bonds: #status Predicted  
Query Match Score 20.0%; DB 1; Length 112;  
Best Local Similarity 28.3%; Pred. No. 7.5E-08;  
Matches 25; Mismatches 35; Indels 19; Gaps 4;  
C:Species: Homo sapiens (man)  
C:Accession: S10216; 60004; JL005; A33400; S02754; A01270; A24434; S12288; A32732; A  
R.Abrahamson, M.; Olaisson, I.; Palsson, A.; Lundwall, A.; Jansson, C.  
Biochem. J. 268, 287-294, 1990  
A:Title: Structure and expression of the human cystatin C gene.  
A:Accession: S10216  
A:Molecule type: DNA  
A:Residue: 1-146 <DNA>  
A:Cross-references: ENBL:X52255; NID:930257; PMID:CRA36497\_1; PMID:G296643  
R.Abrahamson, M.; Grubb, A.; Olafsson, I.; Lundwall, A.  
PEBS Lett. 216, 229-233, 1987  
A:Title: Molecular cloning and sequence analysis of cDNA coding for the precursor of t  
A:Reference number: S00004; MUID:8719149; PMID:345457  
A:Reference number: S00004; MUID:8719149; PMID:345457

A;Accession: S00004  
A;Molecule type: mRNA  
A;Residues: 1-146 <AB2>  
A;Cross-references: EMBL:X05607; PID:gi10371; PID:9755738  
R;Levy, E.; Lopatin, C.; Ghiso, J.; Gaitner, D.; Prangione, B.  
J. Exp. Med. 169, 171-177, 1989  
A;Title: Stroke in Icelandic Patients with hereditary amyloid angiopathy is related to a  
A;Reference number: ULC0095; MUID:8235594; PMID:2541223  
A;Accession: JU0095  
A;Molecule type: DNA  
A;Residues: 1-146 <LEV>  
A;Cross-references: GB:X61681; NID:gi930167; PID:CAA43856; PID:94490944  
A;Note: the cystatin C gene isolated from the brain of an Icelandic patient with heredit  
A;Reference number: A31400; MUID:89350949; PMID:2764935  
A;Molecule type: DNA  
A;Residues: 1-24 T 26-146 <SAI>  
A;Cross-references: GB:MM27889; GB:MM27890; GB:MM27891; NID:gi181385; PID:AAAS2164.1; PID:9  
R;Ghiso, J.; Cowan, N.; Prangione, B.  
Biol. Chem. Hoppe-Seyler's Z. Physiol. Chem. 362, 1324-1331, 1989  
A;Title: Isolation of a sequence encoding human cystatin C. Conservation of exon-intron  
A;Accession number: 802751; MUID:83076307; PMID:3264504  
A;Molecule type: DNA  
A;Accession: 82-119 <GH2>  
A;Cross-references: EMBL:N27769  
A;Note: the authors translated the codon ACC for residue 105 as Thr; the sequence shown  
R;Grub, A.; Lofberg, H.  
Proc. Natl. Acad. Sci. U.S.A. 79, 3024-3027, 1982  
A;Title: Human Gamma-trace, a basic microprotein: amino acid sequence and presence in th  
A;Reference number: A01270; MUID:8222268; PMID:621552  
A;Accession: A01270  
A;Molecule type: protein  
A;Residues: 27-131, S 133-146 <GRU>  
R;Ghiso, J.; Jansson, O.; Prangione, B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2974-2978, 1986  
A;Title: Amyloid fibrils in hereditary cerebral hemorrhage with amyloidosis of Iceland  
A;Reference number: A54534; MUID:86206076; PMID:3517880  
A;Accession: A25334  
A;Molecule type: protein  
A;Residues: 37-93, Q 95-146 <GHI>  
R;Turk, V.; Brin, J.; Longer, M.; Ritonja, A.; Brodin, M.; Borchart, U.; Machleidt, W.  
Hoppé-Seyler's Z. Physiol. Chem. 364, 1487-1496, 1983  
A;Title: Protein inhibitors of cysteine proteinases. III. Amino-acid sequence of cystat  
A;Reference number: S01461; MUID:84110059; PMID:6662498  
A;Accession: S12288  
A;Molecule type: protein  
R;Brzin, J.; Popovic, T.; Turk, V.  
Biochem. Biophys. Res. Commun. 116, 103-109, 1984  
A;Title: Human cystatin, a new protein inhibitor of cysteine proteinases.  
A;Reference number: A32732; MUID:84128015; PMID:6365094  
A;Accession: A32732  
A;Molecule type: protein  
A;Residues: 27-76 <BNZ>  
R;Glaesson, I.; Gudmundsson, G.; Abrahamson, M.; Jansson, O.; Grubb, A.  
Scand. J. Clin. Lab. Invest. 50, 85-93, 1990  
A;Title: The amino terminal portion of cerebrospinal fluid cystatin C in hereditary cys  
A;Reference number: A60532; MUID:90193615; PMID:2315647  
A;Accession: A60532  
A;Molecule type: protein  
A;Residues: 27-49, 52-64 <OLA>  
A;Note: this protein purified from cerebrospinal fluid of patients with the autosomal d  
A;defective gene is not present in CSF but is found instead in amyloid deposits  
R;Popovic, T.; Brzin, J.; Ritonja, A.; Turk, V.  
Biol. Chem. Hoppe-Seyler's Z. Physiol. Chem. 371, 575-580, 1990  
A;Title: Different forms of human cystatin C.  
A;Reference number: S10337; MUID:8831320; PMID:3044831  
A;Accession: S10337  
A;Molecule type: protein  
A;Molecule type: protein  
A;Residues: 27-53 <POP>  
A;Experimental source: urine, kidney disease  
A;Note: truncated form with amino ends at positions 35 and 36 of the precursor were als  
R;Grubb, A.; Lofberg, H.; Barrett, A.J.  
PEBS Lett. 170, 370-374, 1984  
A;Title: The disulphide bridges of human cystatin C (gamma-trace) and chicken cystatin.  
A;Reference number: S01462  
A;Contents: annotation, disulfide bonds  
R;Berti, P.J.; Storer, A.C.  
Biochem. J. 302, 411-416, 1994  
A;Title: Local pH-dependent conformational changes leading to proteolytic susceptibility  
A;Reference number: 655305; MUID:8032991  
A;Accession: 655305  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 27-49106-146 <BER>  
A;Comment: This protein is found in the post-gamma-globulin fraction of cerebrospinal fl  
f patients with certain autoimmune diseases.  
C;Comment: This protein is an inhibitor of cysteine proteinases and may serve an importa  
C;Comment: A mutant cystatin C, with 94-Gln, is deposited in hereditary cerebral hemorrh  
C;Genetics:  
A;Gene: GNB1; OMIM:105150  
A;Cross-reference: GDB:119817; OMIM:105150  
A;Map position: 20p11.2-20p11.12  
A;Introns: 81/3; 119/3  
C;Superfamily: cystatin; cystatin homology  
C;Keywords: amyloid; cysteine proteinase inhibitor; extracellular protein: hydroxyprolin  
P/1-26/Domain: signal sequence #status predicted <SIG>  
P/27-146/Domain: cystatin C #status experimental <MAT>  
P/35-146/Domain: cystatin homology <CTS>  
P/81-85/Region: inhibitory #status predicted  
P/29/Modified site: hydroxylproline (Pro) (partial) #status experimental  
P/99-109, 123-143/Disulfide bonds: #status experimental  
Query Match Score 19.31; Length 146;  
Best Local Similarity 27.0%; Pre: 2.9e-05;  
Matches 33; Conservative 25; Mismatches 53; Indels 11; Gaps 4;  
Qy 8 QPPRKICGGCPDIPNTNSPLEELTHITKLNAAENATPFKDNVKEARVQVAGCKY 67  
Db 31 KPPR--IVCGMDAYSEEEVRLDPAVGETYKNSALQWYARKQIVRAGCKY 88  
Qy 68 FIDPVARETTCSKESNEBLTESC--ETTKLQGSLICNAEVYVWKKIYPPVTVNHWB 124  
Db 89 FLOVEGLGRITCK-.TOPNDNCPPHDOPHLKRKACPSFOIAYVPMQ---GTMTLKST 142  
A;Title: The cDNA structure and expression analysis of the genes for the cysteine protease  
A;Reference number: 807085; MUID:90052122; PMID:2689174  
A;Accession: S07085  
A;Molecule type: mRNA  
A;Residues: 1-127 <>  
A;Cross-reference: EMBL:IX16957; NID:956041; PID:CAA34831.1; PMID:9736290  
R;Barard, A.; Barard, F.; Pucher, D.; Gauthier, F.; Schre  
R;Cole, T.; Dickson, P.W.; Banard, P.; Averill, S.; Risbridger, G.P.; Gauthier, F.; Schre  
Bur. J. Biochem. 186, 35-42, 1989  
A;Title: Two rat homologues of human cystatin C.  
A;Reference number: S01337  
A;Accession: S01337  
A;Molecule type: protein  
A;Molecule type: protein  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 01-Dec-1993 #Sequence Revision 03-Aug-1995 #Text\_change 16-Jul-1999  
C;Accession: S01337; S2109  
R;Turk, V.; Brin, J.; Longer, M.; Ritonja, A.; Brodin, M.; Borchart, U.; Machleidt, W.  
Hoppé-Seyler's Z. Physiol. Chem. 364, 1487-1496, 1983  
A;Title: Protein inhibitors of cysteine proteinases. III. Amino-acid sequence of cystat  
A;Reference number: S01461; MUID:84110059; PMID:6662498  
A;Accession: S12288  
A;Molecule type: protein  
R;Brzin, J.; Popovic, T.; Turk, V.  
Biochem. Biophys. Res. Commun. 116, 103-109, 1984  
A;Title: Human cystatin, a new protein inhibitor of cysteine proteinases.  
A;Reference number: A32732; MUID:84128015; PMID:6365094  
A;Accession: A32732  
A;Molecule type: protein  
A;Residues: 27-76 <BNZ>  
R;Glaesson, I.; Gudmundsson, G.; Abrahamson, M.; Jansson, O.; Grubb, A.  
Scand. J. Clin. Lab. Invest. 50, 85-93, 1990  
A;Title: The amino terminal portion of cerebrospinal fluid cystatin C in hereditary cys  
A;Reference number: A60532; MUID:90193615; PMID:2315647  
A;Accession: A60532  
A;Molecule type: protein  
A;Residues: 27-49, 52-64 <OLA>  
A;Note: this protein purified from cerebrospinal fluid of patients with the autosomal d  
A;defective gene is not present in CSF but is found instead in amyloid deposits  
R;Popovic, T.; Brzin, J.; Ritonja, A.; Turk, V.  
Biol. Chem. Hoppe-Seyler's Z. Physiol. Chem. 371, 575-580, 1990  
A;Title: Different forms of human cystatin C.  
A;Reference number: S10337; MUID:8831320; PMID:3044831  
A;Accession: S10337  
A;Molecule type: protein

A) Residues: 8-49 <B28>  
 R: Esnard, A.; Bonard, P.; Guillou, P.; Gauthier, F.  
 P2BS Lett., 300, 131-135, 1992  
 A/Title: Production of the cysteine proteinase inhibitor cystatin C by rat Sertoli cells  
 A/Reference number: S21109, PMID:92245121, MUID:1563513  
 A/Accession: S21109  
 A/Molecule type: Protein  
 A/Residues: 8-'XX'11-20 <E62>  
 C/Supfamily: cystatin, cystatin homology  
 C/Keywords: cystatin, cysteine proteinase inhibitor  
 P/16-127/Domain: Cystatin homology <C18>  
 P/80-90:104-124/Disulfide bonds: #strands Predicted  
 Query Match      Score 130, DB 2, Length 127,  
 Basic Local Similarity 28.0%, Prcd. No. 4.3e-15/  
 Matches 30, Conservative 28, Mismatches 43, Indels 6, Gaps 4;  
 Qy      8 QPPTKICVGCPRIDPTNSPLEETLTTITKLAENNATTPKIDNTVKARYQVYAGKKV 67  
 Db      11 RPPPRLL-LGAQEAQADASEEGVQALDFAVSBNKGNDAAVHSRAIQVTRARQLVAGINY 69  
 Qy      68 PDPFVARBTTCSESNEBLTSC---ETTKLQGSLDQNAEVYYVPMW 111  
 Db      70 YLDVEMGRITCK-SQTNLIT-NCPFDOPHLRKALCSFQIYSUPWK 114

Search completed: September 24, 2004, 14:10:49  
 Job time : 14.716 secs

Gencore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:08:41 | Search time 44.704 Seconds  
(without alignments)  
913.519 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSDKDFVQPPTRKICVGCPRD.....VWKRKLYPTVTNWKCEP 127

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1149238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 Published Applications AA:\*

1: /cgn2\_6/podata/1/pubpaas/us007\_pubcomb.pep:\*

2: /cgn2\_6/podata/1/pubpaas/us007\_pubcomb.pep:\*

3: /cgn2\_6/podata/1/pubpaas/us007\_new\_pub.pep:\*

4: /cgn2\_6/podata/1/pubpaas/us006\_pubcomb.pep:\*

5: /cgn2\_6/podata/1/pubpaas/us007\_new\_pub.pep:\*

6: /cgn2\_6/podata/1/pubpaas/us005\_pubcomb.pep:\*

7: /cgn2\_6/podata/1/pubpaas/us008\_new\_pub.pep:\*

8: /cgn2\_6/podata/1/pubpaas/us008\_pubcomb.pep:\*

9: /cgn2\_6/podata/1/pubpaas/us009\_pubcomb.pep:\*

10: /cgn2\_6/podata/1/pubpaas/us009\_new\_pub.pep:\*

11: /cgn2\_6/podata/1/pubpaas/us009\_pubcomb.pep:\*

12: /cgn2\_6/podata/1/pubpaas/us009\_new\_pub.pep:\*

13: /cgn2\_6/podata/1/pubpaas/us100\_pubcomb.pep:\*

14: /cgn2\_6/podata/1/pubpaas/us100\_pubcomb.pep:\*

15: /cgn2\_6/podata/1/pubpaas/us100\_new\_pub.pep:\*

16: /cgn2\_6/podata/1/pubpaas/us100\_new\_pub.pep:\*

17: /cgn2\_6/podata/1/pubpaas/us60\_new\_pub.pep:\*

18: /cgn2\_6/podata/1/pubpaas/us60\_pubcomb.pep:\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	61.8	90.0	390	15 US-10-162-331-82 Sequence 82, APP1
2	61.8	90.0	398	15 US-10-162-331-70 Sequence 70, APP1
3	61.8	90.0	427	10 US-09-919-038-29 Sequence 29, APP1
4	61.8	90.0	615	15 US-10-162-331-72 Sequence 72, APP1
5	61.8	90.0	644	15 US-10-162-331-74 Sequence 74, APP1
6	61.8	90.0	644	15 US-10-162-331-84 Sequence 84, APP1
7	381	55.5	424	14 US-10-316-251-217 Sequence 217, APP1
8	390	55.1	430	14 US-10-316-251-215 Sequence 215, APP1
9	163.5	23.8	145	14 US-0-323-423-2 Sequence 2, APP1
10	163.5	23.8	167	10 US-09-744-781-197 Sequence 197, APP1
11	163	23.7	178	9 US-09-969-834-1 Sequence 1, APP1
12	138.5	20.2	121	9 US-09-775-932-14 Sequence 14, APP1
13	138.5	20.2	125	12 US-09-775-932-12 Sequence 12, APP1
14	138.5	20.2	149	9 US-09-940-497-2 Sequence 2, APP1
15	137.5	20.0	112	8 US-08-849-303-16 Sequence 16, APP1

## ALIGNMENTS

RESULT 1  
US-10-162-335-82  
/ Sequence 82, Application US/10162335  
/ General Information:  
/ Publication No. US2004009480A1  
/ Applicant: Anderson, David W.  
/ Applicant: Baumgartner, Jason C.  
/ Applicant: Boilodog, Ferenc L.  
/ Applicant: Casman, Stacie J.  
/ Applicant: Edinger, Shlomit R.  
/ Applicant: Gangoli, Esha A.  
/ Applicant: Gerlach, Valerie  
/ Applicant: Gorman, Linda  
/ Applicant: Guo, Xiaojia (Sasha)  
/ Applicant: Hajit, Tord  
/ Applicant: Keruda, Ramesh  
/ Applicant: Li, Li  
/ Applicant: MacDougall, John R.  
/ Applicant: Mayanay, Uriel M.  
/ Applicant: Millet, Isabelle M.  
/ Applicant: Padigaru, Murajidhara  
/ Applicant: Paturjan, Meera  
/ Applicant: Peña, Carol E. A.  
/ Applicant: Rastelli, Luca  
/ Applicant: Shimkets, Richard A.  
/ Applicant: Stone, David J.  
/ Applicant: Sporek, Kimberly A.  
/ Applicant: Vernet, Corine A. M.  
/ Applicant: Voss, Edward Z.  
/ Applicant: Zethusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Met Peptide Reference: 21402-777 B

PATENT REFERENCE: 21402-777 B

CURRENT APPLICATION NUMBER: US/10162-335

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/295,607

PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/295,651

PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/296,404  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/296,418  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/297,414  
 PRIOR FILING DATE: 2001-06-11  
 PRIOR APPLICATION NUMBER: 60/297,567  
 PRIOR FILING DATE: 2001-06-12  
 PRIOR APPLICATION NUMBER: 60/298,285  
 PRIOR FILING DATE: 2001-06-14  
 PRIOR APPLICATION NUMBER: 60/298,556  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/299,949  
 PRIOR FILING DATE: 2001-06-21  
 PRIOR APPLICATION NUMBER: 60/300,883  
 PRIOR FILING DATE: 2001-06-26  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 201  
 SEQ ID NO: 82  
 LENGTH: 390  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-162-335-82

Query Match 90.0%; Score 618; DB 15; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-59;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 62  
 Db 216 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 275  
 Qy 63 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 118  
 Db 276 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 331

RESULT 2  
 Sequence 70, Application US/10162335  
 Publication No. US2004009480A1  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, David W.  
 APPLICANT: Baumgartner, Jason C.  
 APPLICANT: Boldog, Ferenc L.  
 APPLICANT: Casman, Scacie J.  
 APPLICANT: Seigner, Shomit R.  
 APPLICANT: Gangolli, Bha A.  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Gorman, Linda  
 APPLICANT: Guo, Xiaojia (Sasha)  
 APPLICANT: Hajalt, Tord  
 APPLICANT: Kekudi, Rameesh  
 APPLICANT: Li, Li  
 APPLICANT: MacDougall, John R.  
 APPLICANT: Maliankar, Urel M.  
 APPLICANT: Miller, Isabelle  
 APPLICANT: Padisaru, Muralidhara  
 APPLICANT: Patturajan, Meera  
 APPLICANT: Pina, Carol E. A.  
 APPLICANT: Rastelli, Luca  
 APPLICANT: Shimkets, Richard A.  
 APPLICANT: Stone, David J.  
 APPLICANT: Spyrek, Kimberly A.  
 APPLICANT: Verne, Covine A. M.  
 APPLICANT: Voss, Edward Z.  
 APPLICANT: Zerhusen, Bryan D.  
 TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
 FILE REFERENCE: 21402-377 B  
 CURRENT APPLICATION NUMBER: US/10/162,335  
 CURRENT FILING DATE: 2001-10-01  
 PRIOR APPLICATION NUMBER: 60/295,607  
 PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/295,661  
 PRIOR FILING DATE: 2001-06-04  
 PRIOR APPLICATION NUMBER: 60/296,404  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/296,418  
 PRIOR FILING DATE: 2001-06-16  
 PRIOR APPLICATION NUMBER: 60/297,414  
 PRIOR FILING DATE: 2001-06-11  
 PRIOR APPLICATION NUMBER: 60/298,285  
 PRIOR FILING DATE: 2001-06-12  
 PRIOR APPLICATION NUMBER: 60/298,556  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/299,949  
 PRIOR FILING DATE: 2001-06-21  
 PRIOR APPLICATION NUMBER: 60/300,883  
 PRIOR FILING DATE: 2001-06-26  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 201  
 SEQ ID NO: 70  
 LENGTH: 398  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-162-335-70

Query Match 90.0%; Score 618; DB 15; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-59;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 62  
 Db 224 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 283  
 Qy 63 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 118  
 Db 284 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 339

RESULT 3  
 Sequence 70, Application US/0919039  
 Publication No. US2003010871A1  
 GENERAL INFORMATION:  
 APPLICANT: Kaseer, Matthew R.  
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CBLL CULTURES  
 FILE REFERENCE: PA-0015 US  
 CURRENT APPLICATION NUMBER: US/09/919,039  
 CURRENT FILING DATE: 2003-09-09  
 PRIOR APPLICATION NUMBER: 60/222,113  
 PRIOR FILING DATE: 2000-07-28  
 NUMBER OF SEQ ID NOS: 401  
 SOFTWARE: PBRL Program  
 SEQ ID NO: 29  
 LENGTH: 427  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1  
 US-09-919-039-29

Query Match 90.0%; Score 618; DB 10; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-59;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 62  
 Db 263 GKDQVQPTKICGGPRDIPNSPBLETLTITLTKAENNTYFKIDNVKCKARYQQV 312  
 Qy 63 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 118  
 Db 313 AGKRYFDIVARETCSKESNEELTESCTKLQGSDCNAEVYVPMERKKIYPTV 368

RESULT 4  
Sequence 72, Application US/10162335  
Publication No. US20040009480A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edlinger, Shlomit R.  
APPLICANT: Gargoli, Esha A.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaochia (Sasha)  
APPLICANT: Hjalt, Tor  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: Macdougall, John R.  
APPLICANT: Malynkar, Uriel M.  
APPLICANT: Miller, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patta, Carol E. A.  
APPLICANT: Patta, Luca  
APPLICANT: Shimeto, Richard A.  
APPLICANT: Stone, David J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zernhusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
FILE REFERENCE: 21402-377 B  
CURRENT APPLICATION NUMBER: US/10/162,335  
CURRENT FILING DATE: 2004-10-01  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,661  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,404  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,418  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/297,414  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/298,285  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/298,556  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/299,949  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/300,883  
PRIOR FILING DATE: 2001-06-26  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 201  
SEQ ID NO 72  
Length: 615  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-162-335-72

Query Match score 618; DB 15; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1,1e-58;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDFFQPPTKIVCGCPDIPNSPLEETLTTITKNAENNTPKIDNVRARYVQV 62  
Db 224 GKDFFQPPTKIVCGCPDIPNSPLEETLTTITKNAENNTPKIDNVRARYVQV 283  
Qy 63 AGKRYFIDFVARETICSKESENBELETSCTKQGSLDCNAEVYVWMBKRKYPTV 118

RESULT 5  
Sequence 74, Application US/10162335  
Publication No. US20040009480A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edlinger, Shlomit R.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edlinger, Shlomit R.  
APPLICANT: Gargoli, Esha A.  
APPLICANT: Gargoli, Esha A.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaochia (Sasha)  
APPLICANT: Hjalt, Tor  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: Macdougall, John R.  
APPLICANT: Malynkar, Uriel M.  
APPLICANT: Miller, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patta, Carol E. A.  
APPLICANT: Patta, Luca  
APPLICANT: Shimeto, Richard A.  
APPLICANT: Stone, David J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zernhusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
FILE REFERENCE: 21402-377 B  
CURRENT APPLICATION NUMBER: US/10/162,335  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,661  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,404  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,418  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/297,414  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/298,285  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/298,556  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/299,949  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/300,883  
PRIOR FILING DATE: 2001-06-26  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 201  
SEQ ID NO 74  
LENGTH: 644  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-162-335-74

Query Match score 618; DB 15; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1,1e-58;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GKDFFQPPTKIVCGCPDIPNSPLEETLTTITKNAENNTPKIDNVRARYVQV 62  
Db 224 GKDFFQPPTKIVCGCPDIPNSPLEETLTTITKNAENNTPKIDNVRARYVQV 283  
Qy 63 AGKRYFIDFVARETICSKESENBELETSCTKQGSLDCNAEVYVWMBKRKYPTV 118

RESULT 6  
 Sequence 84, Application US/10162335  
 Publication No. US20040094801  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, David W.  
 APPLICANT: Baumgartner, Jason C.  
 APPLICANT: Boidog, Ferenc L.  
 APPLICANT: Caeman, Stacie J.  
 APPLICANT: Edinger, Shomit R.  
 APPLICANT: Gangoli, Zaha A.  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Gorman, Linda  
 APPLICANT: Guo, Xiaojia (Sasha)  
 APPLICANT: Hajal, Tord (Sasha)  
 APPLICANT: Kekuda, Ramash  
 APPLICANT: Li, Li  
 APPLICANT: Macbougall, John R.  
 APPLICANT: Malayankar, Uriel M.  
 APPLICANT: Millet, Isabelle  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Paturajan, Meera  
 APPLICANT: Peña, Carol E. A.  
 APPLICANT: Raselli, Luca  
 APPLICANT: Shimkete, Richard A.  
 APPLICANT: Stone, David J.  
 APPLICANT: Spryek, Kimberly A.  
 APPLICANT: Vernet, Corine A. M.  
 APPLICANT: Voss, Edward Z.  
 APPLICANT: Zethusen, Bryan D.

TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
 FILE REFERENCE: 21102-377-B  
 CURRENT APPLICATION NUMBER: US/10/162,335  
 CURRENT FILING DATE: 2002-10-01  
 PRIOR APPLICATION NUMBER: 60/295,607  
 PRIOR FILING DATE: 2001-06-04  
 PRIOR APPLICATION NUMBER: 60/295,661  
 PRIOR FILING DATE: 2001-06-04  
 PRIOR APPLICATION NUMBER: 60/295,404  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/295,418  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/297,414  
 PRIOR FILING DATE: 2001-06-11  
 PRIOR APPLICATION NUMBER: 60/297,567  
 PRIOR FILING DATE: 2001-06-12  
 PRIOR APPLICATION NUMBER: 60/298,285  
 PRIOR FILING DATE: 2001-06-14  
 PRIOR APPLICATION NUMBER: 60/298,556  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/299,919  
 PRIOR FILING DATE: 2001-06-21  
 PRIOR APPLICATION NUMBER: 60/300,883  
 PRIOR FILING DATE: 2001-06-26  
 Remaining Prior Application data removed - See File Wrapper or PAM.  
 NUMBER OF SEQ ID NOS: 201  
 SEQ ID NO: 84  
 LENGTH: 644  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-162-335-84

Query Match 90.0%; Score 618; DB 15; Length 644;  
 Best Local Similarity 100.0%; Prd. No. 1.e-58;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GRDFQPPTKICVGCPDIPNTSSPELBETLTTKINAENNATPFKIDNVKARVQVV 62

RESULT 7  
 US-10-162-253-217  
 Sequence 217, Application US/1016253  
 Publication No. US20030162706A1  
 GENERAL INFORMATION:  
 APPLICANT: The Procter & Gamble Company  
 APPLICANT: Peters, Kevin  
 APPLICANT: Thompson, Larry  
 APPLICANT: Wang, Peng  
 APPLICANT: Greis, Kenneth  
 APPLICANT: Angiogenesis Modulating Proteins  
 FILE REFERENCE: 8865M  
 CURRENT APPLICATION NUMBER: US/10/316,253  
 CURRENT FILING DATE: 2002-12-10  
 PRIOR APPLICATION NUMBER: US 60/355,295  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 217  
 LENGTH: 424  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-316-253-217

Query Match 55.5%; Score 381; DB 14;  
 Best Local Similarity 62.1%; Prd. No. 5.8e-33;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

3 GRDKQPPTKICVGCPDIPNTSSPELBETLTTKINAENNATPFKIDNVKARVQVV 62  
 DB 246 GDDPELLPKNRCREREIVDSPELKAHGSIARNAOHNHPFKIDTVKAKTSQVV 305

Query Match 55.3%; Score 380; DB 14;  
 Best Local Similarity 62.1%; Prd. No. 7.7e-33;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

3 GRKYPFDVARETCSKESNEBELTSCETKKGOSLDCAEVYVPMWKIYPTV 118  
 DB 313 AGKYPFDVARETCSKESNEBELTSCETKKGOSLDCAEVYVPMWKIYPTV 368

RESULT 8  
 US-10-3-253-215  
 Sequence 215, Application US/1016253  
 Publication No. US20030162706A1  
 GENERAL INFORMATION:  
 APPLICANT: The Procter & Gamble Company  
 APPLICANT: Peters, Kevin  
 APPLICANT: Thompson, Larry  
 APPLICANT: Wang, Peng  
 APPLICANT: Greis, Kenneth  
 APPLICANT: Angiogenesis Modulating Proteins  
 FILE REFERENCE: 8865M  
 CURRENT APPLICATION NUMBER: US/10/316,253  
 CURRENT FILING DATE: 2002-12-10  
 PRIOR APPLICATION NUMBER: US 60/355,295  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 215  
 LENGTH: 430  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-316-253-215

Query Match 55.3%; Score 380; DB 14;  
 Best Local Similarity 62.1%; Prd. No. 7.7e-33;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

3 GKDPEVQPPPTKICVGCGPRDITPSPELETLTTITKNAENATYFKIDNVAEVQVV 62  
 252 GDDPBLPKQRCGPREPVDSEELKALGNSIAQLNQHNRHPIFKIDTUKRSQQV 311  
 63 AGKCKYPIDFVARETCSKSNBNEELTESCTKLGQSOLDCAEVYVVPWKEKPYTV 118  
 312 AGTYVIEPIARTECSKQSKTBLTADCTEKLGSLNCAVNTMRPNENKVPTV 367

## RESULT 9

US-10-339-428-2  
 Sequence 2, Application US/10329428  
 Publication No. US20030114646A1  
 GENERAL INFORMATION:  
 APPLICANT: Lin, et al.  
 TITLE OF INVENTION: Human Cystatin P  
 FILE REFERENCE: PP2465P1D2  
 CURRENT APPLICATION NUMBER: US/10/329,428  
 CURRENT FILING DATE: 2002-12-27  
 PRIOR APPLICATION NUMBER: 60/014,795  
 PRIOR FILING DATE: 1996-04-03  
 PRIOR APPLICATION NUMBER: 08/832,535  
 PRIOR FILING DATE: 1997-04-03  
 PRIOR APPLICATION NUMBER: 09/019,485  
 PRIOR FILING DATE: 1998-01-29  
 PRIOR APPLICATION NUMBER: 09/528,436  
 PRIOR FILING DATE: 2000-03-17  
 NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: Patentin version 3.2  
 SEQ ID NO: 2  
 LENGTH: 145

US-10-339-428-2

Query Match 23.8% Score 163.5% DB 14; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.7e-10; Gaps 3;  
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

Qy 11 TKICVGCGPRDITPSPELETLTTITKNAENATYFKIDNVAEVQVVAGKPYFD 70  
 Db 32 SRVKPGPKTITNDPCVLQAARSVEKENCTNDMLPKESRITRALVOVKGKYM 91  
 Qy 71 FVARETCSKSNBNEELTESC--TKKGQSOLDCAEVYVVPWKEKPYTVNHW 124  
 Db 92 VELGRTECKQHRL-DDCPFTNTLQQTLSYCSEWVWP-----LQHPE 138

## RESULT 10

US-09-746-783-197  
 Sequence 197, Application US/09746783  
 Publication No. US2003044935A1  
 GENERAL INFORMATION:  
 APPLICANT: Jacob9, Kenneth  
 McCoy, John M.  
 Lavalle, Edward R.  
 Racie, Lisa A.  
 Tracy, Maurice  
 Spaulding, Vicki J.  
 Agostino, Michael J.  
 Hayes, Steven H.  
 Fachtai, Kim

TITLE OF INVENTION: SECRETED PROTBINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 211  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: U.S.A.  
 ZIP: 02140  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk;  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/746,783  
 FILING DATE: 21-Dec-2000  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Milasincic, Debra J.  
 REGISTRATION NUMBER: 46,931  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEX/FAX: (617) 742-1214  
 INFORMATION FOR SEQ ID NO: 197:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 167  
 TYPE: amino acid  
 STRANDBEHNESS: <Unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 197:  
 US-09-746-783-197  
 Query Match 23.8% Score 163.5% DB 10; Length 167;  
 Best Local Similarity 31.6%; Pred. No. 1.2e-09; Gaps 45; Indels 13; Gaps 3;  
 Matches 37; Conservative 22; Mismatches 21;  
 Qy 11 TKICVGCGPRDITPSPELETLTTITKNAENATYFKIDNVAEVQVVAGKPYFD 70  
 Db 54 SRVKPGPKTITNDPCVLQAARSVEKENCTNDMLPKESRITALVOVKGKYM 113  
 Qy 71 FVARETCSKSNBNEELTESC--TKKGQSOLDCAEVYVVPWKEKPYTVNHW 124  
 Db 114 VELGRTECKQHRL-DDCPFTNTLQQTLSYCSEWVWP-----LQHPE 160  
 RESULT 11  
 US-09-969-834-1  
 Sequence 1, Application US/0969834  
 Patent No. US2002010271A1  
 GENERAL INFORMATION:  
 APPLICANT: Bandman, Olga  
 Gali, Surya K.  
 TITLE OF INVENTION: Novel Human cystatin-like protein  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSBQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/969,834  
 FILING DATE: 01-Oct-2001  
 CLASSIFICATION: <Unknown>  
 APPLICATION NUMBER: US/09/471,765  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US/08/791,522  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: 09/471,765  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PP-0193 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-845-0555  
 TELEX/FAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 178 amino Acids  
 TYPE: amino acid  
 STRANDBNESS: Single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: 30443  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-969-834-1

Query Match Score 163; DB 9; Length 178;  
 Best Local Similarity 23.7%; Pred. No. 1.4e-09;  
 Matches 35; Conservative 20; Mismatches 44; Indels 8 Gaps 2;

Qy 11 TKICVGCPRDIPTNSPELETLTITKLNAENNTYFKIDNVKARVQVAGKXKPYI 69  
 Db 54 SRVAPGFPKTKITNDPVLQARAYSTEKPANCIDMFLPKESRITALQVIGSLKTYML 113

Qy 71 DFVARETCSKE---SNBELTECETKLGQ--SLDGNAEVVVVWE 111  
 Db 114 VEGRTCKQHHLRL-DDCDFQFTNLKOTLSCESEVWWFW 155

RESULT 12  
 US-09-775-932-14

Sequence 14, Application US/09775932  
 Patent No. US20020137671A1

GENERAL INFORMATION:  
 APPLICANT: University of British Columbia  
 TITLE OF INVENTION: Production and use of Modified Cystatins  
 FILE REFERENCE: 58069  
 CURRENT APPLICATION NUMBER: US/09/775,932  
 CURRENT FILING DATE: 2001-02-02  
 PRIOR APPLICATION NUMBER: CA99/000217  
 PRIOR FILING DATE: 1999-08-05  
 PRIOR APPLICATION NUMBER: 60/095,503  
 PRIOR FILING DATE: 1998-08-05  
 NUMBER OF SEQ ID NOS: 32  
 SEQ ID NO 14  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 121  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-775-932-14

Query Match Score 138.5; DB 9; Length 121;  
 Best Local Similarity 31.5%; Pred. No. 4.2e-07;  
 Matches 34; Conservative 22; Mismatches 45; Indels 8 Gaps 3;

Qy 10 PTKICVGCPRDIPTNSPELETLTITKLNAENNTYFKIDNVKARVQVAGKXKPYI 69  
 Db 2 PQERMVGEGLDLSPPDPQKAQAAVASYNGNSIYYFRDTHIIKAGSOLVAGKXKPYI 61

Qy 70 DFVARETCSKE---SNBELTECETKLGQ--SLDGNAEVVVVWE 111  
 Db 62 TMEMGSTDCRTRVGDHYDLT-TPLLAGAQOEKLRCDFEVLYVPWQ 108

RESULT 13  
 US-09-775-932-12

Sequence 12, Application US/09775932  
 Patent No. US20020137671A1

GENERAL INFORMATION:  
 APPLICANT: University of British Columbia  
 TITLE OF INVENTION: Production and use of Modified Cystatins  
 FILE REFERENCE: 58069  
 CURRENT APPLICATION NUMBER: US/09/775,932  
 CURRENT FILING DATE: 2001-02-02

Query Match Score 138.5; DB 9; Length 128;  
 Best Local Similarity 31.5%; Pred. No. 4.5e-07;  
 Matches 34; Conservative 22; Mismatches 45; Indels 8 Gaps 3;

Qy 10 PTKICVGCPRDIPTNSPELETLTITKLNAENNTYFKIDNVKARVQVAGKXKPYI 69  
 Db 9 PQERMVGEGLDLSPPDPQKAQAAVASYNGNSIYYFRDTHIIKAGSOLVAGKXKPYI 68

Qy 70 DFVARETCSKE---SNBELTECETKLGQ--SLDGNAEVVVVWE 111  
 Db 69 TMEMGSTDCRTRVGDHYDLT-TPLLAGAQOEKLRCDFEVLYVPWQ 136

RESULT 14  
 US-09-940-497-2

Sequence 2, Application US/09940497  
 Patent No. US20020132476A1

GENERAL INFORMATION:  
 APPLICANT: Ni et al.  
 TITLE OF INVENTION: Human Cystatin E  
 FILE REFERENCE: PP02P1D2  
 CURRENT APPLICATION NUMBER: US/09/90,497  
 CURRENT FILING DATE: 2001-08-29  
 PRIOR APPLICATION NUMBER: US 09/241,376  
 PRIOR FILING DATE: 1999-02-02  
 PRIOR APPLICATION NUMBER: US 08/744,138  
 PRIOR FILING DATE: 1996-11-05  
 PRIOR APPLICATION NUMBER: US 08/461,030  
 PRIOR FILING DATE: 1995-06-05  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2  
 LENGTH: 149  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-940-497-2

Query Match Score 138.5; DB 9; Length 149;  
 Best Local Similarity 31.5%; Pred. No. 5.5e-07;  
 Matches 34; Conservative 22; Mismatches 45; Indels 9 Gaps 3;

Qy 10 PTKICVGCPRDIPTNSPELETLTITKLNAENNTYFKIDNVKARVQVAGKXKPYI 69  
 Db 30 PQERMVGEGLDLSPPDPQKAQAAVASYNGNSIYYFRDTHIIKAGSOLVAGKXKPYI 69

Qy 70 DFVARETCSKE---SNBELTECETKLGQ--SLDGNAEVVVVWE 111  
 Db 90 TMEMGSTDCRTRVGDHYDLT-TPLLAGAQOEKLRCDFEVLYVPWQ 136

RESULT 15  
 US-09-844-303-16

Sequence 16, Application US/08849303  
 Publication No. US2003022109A1

GENERAL INFORMATION:  
 APPLICANT: McPherson, Michael J.  
 APPLICANT: Urwin, Peter E.  
 TITLE OF INVENTION: MODIFIED PROBINASB INHIBITORS  
 NUMBER OF SEQUENCES: 79  
 CORRESPONDENCE ADDRESS:

Page 7

ADDRESSEE: Kluber & Jackson  
STREET: 411 Hackensack Avenue, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version 1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,303  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1321-1-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
SEQ ID NO: 849,303-16

Search completed: September 24, 2004, 14:13:04  
Job time : 45.704 secs

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